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AC02717 Homo saptens chr
AC010217 Homo saptens chr
AC010272 Homo saptens chr
AC011940 Homo saptens clo
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Eutheria; Euthates; Catarrhini; Hominidae; Homo.

Primates; Catarrhini; Hominidae; Homo.

1 (basea; 1 to 1318)

Jantzer, P. U. and Schendel, D.J.

Tumor-infiltrating lymphocytes recognizing spontaneously arising Tumor-infiltration appropriate express T cell receptors characteristic of a secondary immune response
Unpublished
                                                                                                                                                                                                                       J gene; junction; T cell receptor; TCR junctional sequence; V gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (11-JUN-1996) P. Jantzer, Institute for Immunology, Goethestr. 31, D- 80336 Munich, FRG Goethestr. 31, Location/Qualifiers
                                                                                                                                                        08-JAN-1997
                                                                                                                                                                           H.sapiens mRNA for rearranged TCR junctional sequences
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/codon_start=1
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5.1e+03
5.5e+03
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08-881509-7 x HSTCRJUNC
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                                        gb_htg13:AC027717
gb_htg3:AC010217
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gb_htg4:AC011940
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AL359961 Homo sapiens chromd
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i AC073696 Mus musculus clone
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-WODEL-frame+_D2n.model -DEV-x1P -881509/runat_28032001_092236_29744/app_query.fasta_1.
-WODEL-frame+_D2n.model -DEV-x1P -881509/runat_28032001_092236_29744/app_query.fasta_1.
-O-/C9n2_1/USPTO_spool/DECLOUX.08-081509/runat_000 -GAPEXT-4.000
-O-/C9n2_1/USPTO_spool/DECLOUX.08-000 -GAPEXT-4.000
-NINMATCH-0.100 -LOOPCL-0.000 -LOOPCT-0.000 -FGAPOP-6.000
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-EGAPEXT-7.000 -START-1 -MATRIX-blosamed_TRANS-human40.cdi
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-MAXLEN-2000000000 -USER-DECLOUX.08-981509_GCGNI_1.5287
-NGPU-6 -ICPU-3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                          About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Database length: 1736092196
Search time (sec): 3669.890000
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Query: 08-881509-7
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gb_htg10:AC023806
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gb_htg17:AC073732
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gb_pat1:A93133
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gb_ba2:PP2ABLIGG
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gb_pr6:HS41018
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gb_htg15:AC064575
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gb_htg8:AC021520
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gb_htg8:AC021669
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                                                                                                                                    Date: Apr 1, 2001
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LOCUS S69140 98 bp mRNA PRI 23-SEP-1994
DEFINITION TCR V alpha-T-cell receptor alpha-chain (allergen-specific) [human, grass-sensitive individual VI 19, Peripheral blood, mRNA Partial,
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Mohapatra, S.S., Mohapatra, S., Yang, M., Ansari, A.A., Parronchi, P., Molecular basis of cross-reactivity among allergen-specific human T Immunology 81 (1), 15-20 (1994)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="This sequence comes from Fig. 3b; Protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 144562] from the original journal article.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human peripheral blood grass-sensitive individual VI 19.
                                                                                                                                                                                                                                                                                                                                                            Gaps: 0
Percent Identity: 84.615
                                                                                                                                                                                            /note="unnamed protein product"
                                                                  T-cells specific for kidney carcinome Patent: EP 0816496-A 07-JAN-1998; BOEHRINGER MANNHEIM GMBH (DE)
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                                                                                                                                                               /db_xref="taxon:32644"
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                                                                                                                     Location/Qualifiers
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              unidentified
unclassified.
[ (bases 1 to 39)
schendel, D.J.
                                                                                                                                                                                                                                                                                                                                                          Percent Similarity: 100.000
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SOSKDSDVYITDKTVLDMRSNDFKSNGAVAWSNKSDFACANAFNNSIIPEDDTFPSDFY
SSCDVKLVEKSFFETDTNLNFQNLSVIGFRILLKVAGFNLLMTLRLWSS"
         is in conflict with the conceptual translation"
                                                                                                                                                                   Percent Similarity: 85.714 Percent Identity: 78.571
                                                                                                                                                                                                                                                                                    16 TTCTGTGCAGCCTTACCTGGTTCTGCAAGGCAACTGACCTTT 57
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Percent Identity: 78.571
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Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
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A93127
A93127.1 GI:6741516
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/db_xref="taxon:32644"
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                                                                                                                                                                                                                                                                                                                                                                  1341 bp
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Schendel, D. J.
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unidentified
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08-881509-7 x A93127
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                                                                                                                                                                                                          alignment_block;
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                                                                                          BASE COUNT
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VERSION
KEYWORDS
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REFERENCE
AUTHORS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 18 clone RP11-129F9 map 18, WORKING DRAFT SEQUENCE, 15 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clonal expansion of myelin basic protein-reactive T cells in patients with multiple sclerosis: restricted T cell receptor V gene rearrangements and CDR3 sequence

Fur. J. Immunol. 25 (4), 958-968 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 87) (bases 1 to 87)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Partial TCRVA (1. 15), TCRNA (16. 18), TCRJA (19. 75), partial TCRCA (76. 87)" /codon_start=1
                                                                                                                                                           DUCUS HUMTCRACG 87 bp mRNA PRI 07-NOV-1995
DEFINITION Homo sapiens (clone NS1-F4) T cell receptor alpha chain (TCRA)
MRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="YFCAEASGSARQLTFGSGTQLTVLPDIQK"
19 c 21 g 27 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="GDB:G00-120-404"
/product=T_Cell receptor alpha chain"
/protein_id="AAA80964.1"
/db_xref="GI:853663"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 64.286
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                                 L42801.1 GI:853662
L42801.1 Cell receptor alpha.
Homo sapiens (clone: NS1-F4) cDNA to mRNA.
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo saplens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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LOCUS AC021669 157437 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="NS1-F4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="TCRA"
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08-881509-7 x HUMTCRACG
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                                                                                                                                         seq_name: gb_pr8:HUMTCRACG
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Percent Similarity:
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MEDLINE
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2. (bases 1 to 157437)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barren, B., Linton, L., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Boukhgalter, B., Brown, A., Burkett, G., Coste, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, M., Porrest, C., Gangan, J., Gard, G., Hagos, B., Heaford, A., Horton, L., Landers, P., ItzHugh, M., Porrest, C., Liu, G., Locke, K., Landers, T., Lehoczky, J., Leylne, R., Jones, C., Marn, L., Marlans, A., Kland, J., Mardan, J., Mardan, D., McPheeters, R., Mardin, J., Meneus, L., Morrow, J., Naylor, J., McPheeters, R., Meldrin, J., Meneus, L., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. H., Peterson, K., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pollara, V., Subcamanian, R., Talamas, J., Tesfaye, S., Theodore, J., Stimmer, A., and Zody, M., Viel, R., Wo, A., Wu, X., Myman, D., Ye, W.J., Limmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (19-Jan-2000) Whitehead Institute/MIT Center for Genome Submitted (19-Jan-2000) Whitehead Institute/MIT Center for Genome Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
All repeats were identified using RepeatMasker:
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://fp.genome.washington.edu/RM/RepeatMasker.html
http://fp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. The record will be updated with the finished sequence russ record will be updated with the accession number will as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: wnitenedu instituto, nit center code: wire the code: with the code code: with the contact: sequence_submissions@genome.wi.mit.edu contact: sequence_submissions@genome.wi.mit.edu conter project information

Center project name: 1230
Center clone name: 1230
Center clone name: 125F_F_9
Center clone name: 125F_F_9
Center clone name: 125F_F_9
Center clone name: 125F_F_9
Center clone name: 125C_F_9
Center clone n
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49008: contig of 9922 bp in length
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5817: contig of 2683 bp in length
gap of unknown length
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21956: contig of 7052 bp in length
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3134: contig of 1838 bp in length
gap of unknown length
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gap of unknown length
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gap of unknown length
1 (bases 1 to 157437)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Birmen,B., Linton,L., Nusbaum,C. and Lander,E.
Grown sapiens chromosome 18, clone RP11-129F9
Unpublished
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; RS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Mazny, D. M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Budocka, B., Bouck, J., Bowies, A., Buday, C., Buracc, C., David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N., Forcum-Tansey, J., Frantz, P., Carter, M., Carcia, D. K., Gorrell, D., Gorrell, L., Guevara, W., Harist, K., Hex., Hernandez, J., Gorrell, L., Guevara, M., Harist, K., Hex., Harrandez, J., Gorrell, J. H., Jackson, A., Hogues, M., Holly, S., Kondejewski, N., Kong, Y., Lozado, R., Mores, M., Kelly, S., Kondejewski, N., Kong, Y., Lozado, R., Mortis, C., Liu, J., Liu, W., Logan, O., Nelson, A., Mouven, R., Martin, R., Martinez, C., Mash, S., Moorish, T., Morgan, M., Morris, S., Nash, S., Barter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E., Shen, H., Vasquez, L., Vinson, R., Wayuen, S., Scherer, S., Shah, E., Shen, H., Vasquez, L., Vinson, R., Volo, Wahbah, M., Watlington, S., Taylor, T., Werensford, G., Yu, W., Zhou, X., Naylor, S.L., Nelson, S., Ur, W., Sparks, A., Stamps, A., Wallianson, A., Worley, K., Wren, J., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      __documentation_block:
US AC009319 172581 bp DNA PRI 11-OCT-2000
INITION Homo sapiens 3 BAC RPI1-297K7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
gap of unknown length
74733: contig of 13479 bp in length
74733: contig of 1246 bp in length
gap of unknown length
89274: contig of 12246 bp in length
104301: contig of 14541 bp in length
gap of unknown length
123037: contig of 15027 bp in
123037: contig of 18736 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
3 157437: contig of 18736 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="RP11-129F9"
/clone_lib="RPCI-11 Human Male BAC"
39877 a 39144 c 38679 g 39736 t l others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: AC021669 from: 1 to: 157437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="18"
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85.714
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Ratio:
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Worley, K.C.
Direct Submission
Submitted (16-AUG-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One 3 (bases 1 to 172581)
                                                                                                                                                                                                                               Submitted (28-JUL-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One (bases 1 to 172581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-Aug-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One (bases 1 to 172581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (25-Aug-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, Tx 77030, USA
ON 5701 28, 2000 this sequence Version replaced gi:9438826.
gc-help@bcm.tnc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANNOTATION OF FEATURES:
STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nepeats are incirition using nepeatinases (n. Smit and F. Green, Genes and Region of Sequences.

(Nuc. Acids Res. 25:3389-3402) similarity are identified by BLAST EST and CDNA Sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice sites that maintained sequence identical matches are annotated as similar.
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/note="Unigene cluster similar to: SEG_HSLPP Human lipoma
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938. .6929
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        (bases 1 to 172581)
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784. 825
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                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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complement(25074. .25376)
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25419. .25705
preferred partner (LPP) gene"
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4843.
                                                                                                                                                                                                      family="Alux"
5. .126?
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24159. 2446
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                                                                             /rpt_family="Alux"
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7630. .7677
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complement(11625...
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                                                                              complement(8904.
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Mammalla; Eutinetra; Filimates, Colling Parabaria, J., Blankenburg, K., Radams, C., Bailey, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C., Bouck, J., Carter, M., Chacko, J., Chen. Z., Cox, C., Borrack, C., Burrows, J., Carter, M., Chacko, J., Chen. Z., Cox, C., Cox, Cox, Cox, Dayan-Rocha, S., Durbin, K. J., Fernandez, C., Ferraguto, D., Dugan-Rashid, N., Pantz, P., Frantz, P., Hondson, A., Hogues, M., Harris, K., Hernandez, J., Hodgson, A., Hogues, M., Harris, K., Hernandez, J., Hodgson, A., Hogues, M., Harris, K., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hosak, H., Jackson, L.E., Jackson, L.E., Jackson, L. Lu, J., Lu, J., Lichtarge, O., Liu, J., Liu, Kong, Y., Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Liu, Martinez, C., McLeod, M.P., Meilo, S., Nash, S., Samuel, S., Say, J., Scherer, S., Quiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Quiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Vash, B., L., Vasqiez, L., Vilison, R., Vo, C., Wahbah, M., Tabor, P., Taylor, T., Vasqiez, L., Vilison, R., Vo, C., Wahbah, M., Walley, S., Weinstock G., Weinstock, I. R., Williamson, A., Weilber, V., Wren, J., Williamson, A., Shan, S., Nash, S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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LOGUS #AC48847 175814 bp DNA
LOGUS #AC48847 175816 bb.hromosome 12 clone RP11-367G12, WORKING DRAFT
DEFINITION Homo sapiens chromosome 12 clone RP11-367G12, WORKING DRAFT
SEQUENCE, 19 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TyrcysLeuAlaLeuAlaGlySerAlaArgGlnLeuThrPhe 14
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32348. 32360
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complement(33728. 34028)
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28306. .28067
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Direct Submission
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Ratio: 4.083
Percent Similarity: 85.714
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08-881509-7 x AC009319
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AUTHORS TITLE JOURNAL

COMMENT

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FEATURES
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                                   Submitted (14-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                      Chemistry: Dye-primar Bodipy: 28% of reads
Chemistry: Dye-terminator Big Dye: 72% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 155020 bases at least 040
Consensus quality: 15521 bases at least 020
Estimated insert size: 170493; sum-of-config estimation
Quality coverage: 0x in 020 bases; sum-of-config estimation
Quality coverage: 3.6x in 020 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.hgsc.bcm.tmc.edu/doss/Genbank_draft_data.html).

NOTE: This is a working draft' sequence. It currently consists of 19 contigs. The true order of the pieces arbitrary. Gaps between the contigs are represented as rous of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: Estimated insert size may differ from sequence length
                                                                      Baylor Plaza, Houston, TX 77030, usa on Aug 31, 2000 this sequence version replaced gi:9930656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of unknown length
contig of 15195 bp in length
gap of unknown length
contig of 15080 bp in length
gap of unknown length
contig of 10474 bp in length
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is contig of 10042 ...
is gap of unknown length
7: contig of 5244 bp in length
77: gap of unknown length
77: gap of unknown length
77: gap of 1433 bp in length
77: fin of 7433 bp in length
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contig of 26949 bp in length
gap of unknown length
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contig of 21001 bp in length
are of unknown length
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known length
10042 bp in length
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of 3436 bp in length
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                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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of 5490 bp in l
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gap of unknown 1
                                                                                                                                                                                                                     ---- Project Information
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                                                                                                                                                         Center code: BCM
Worley, K.C.
Direct Submission
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173981
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Expansion in the control of the cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (22-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 31, 2000 this sequence version replaced gi:9280749.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                            1828 others
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Contact: sequence_submissions@genome.wi.mit.edu
Project Information
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                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-367G12"
50954 a 35383 c 35133 g 52516 t
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Location/Qualifiers
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Center clone name: 1_B_18
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                             source
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ORGANISM
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consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as some as it is available and the accession number will
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228999: contig of 20225 bp in length
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128829: contig of 24247 bp in length
18929: gap of 100 bp
145919: contig of 16990 bp in length
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100 bp
570: contig of 7993 bp in length
670: gap of
67050: conti
                                                                                                                                                                                                                                                        184 2283: gap of 100 bp 2184 2893: gap of 2184 2893: gap of 100 bp 2884 5870: contig of 3587 bp in length
                                                                                                                                                                                                                                                                                                  2184 2283: gap of 100 bp 2284 5870: contig of 3587 bp in length 5871: gap of 100 bp 5871 13493: contig of 7523 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                           93: gap of 100 bp 20146: contig of 6553 bp in length
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Percent Identity: 64.286
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/db_xref="taxon:9606"
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190362: conti
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146020 176141: cont
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Percent Similarity: 85.714
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08-881509-7 x AC010758
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2 (bases 1 to 73806)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 73806)
                                                                                                                                                                                                                                                               Submitted (15-OCT-1998) Cross S.M., Queensland Institute of Medical Research, The Bancroft Centre, 300 Herston Road, Brisbane,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACULES 20 73806 bp DNA HTG 13-JUL-2000 HTG 13-JUL-2000 SEQUENCE STRONG SET 17. LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                       Disses 1 to 42)
Misko, I.S., Cross, S.M., Khanna, R., Elliott, S.L., Schmidt, C.,
Misko, I.S., Cross, S.M., Khanna, R., Elliott, S.L., Schmidt, C.,
Pye, S.J. and Stonghilton of viral, self, and bacterial peptide crossreactive recognition of viral, self, and bacterial peptide crossreactive recognition of viral, self, and bacterial peptide ligands by human class I-restricted cytotoxic T lymphocyte clonotypes: implications for molecular minitory in autoimmune
HSA235208 42 bp mRNA HORD SAPION 12-WAR-1999 HOMO SAPIENS MRNA for T cell receptor alpha chain V-J junctional region (TCRAV7AJ16S3).
                                                                                                                r cell receptor; T cell receptor alpha chain; variable region.
                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 42)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 96 (5), 2279-2284 (1999)
99162595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="cytotoxic T lymphocyte"
/cell_line="SP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/haplotype="Al, A2, B8, B45, Bw6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CysLeuAlaLeuAlaGlySerAlaArgGlnLeuThrPhe 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo saplens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="blood"
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AC021520.2 GI:9148483
HTG; HTGS_PHASE0.
                                                                                                          AJ235208.1 GI:3851223
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Percent Similarity: 92.308
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LOCUS AC021520
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08-881509-7 x HSA235208
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6
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REFERENCE
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                                                                                                                              VERSION
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Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Chopel, Y. Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Howland, J.C., Johnson, B., Hadford, A., Horton, L., Landers, T., Lehocsky, J., Levins, C., Kann, L., Karatas, A., Klein, J., Marduis, N., McDwan, P., McGurk, A., McKernan, K., McPheters, R., Marquis, N., McDwan, P., McGurk, A., McKernan, K., Norman, C. H., O'Connor, T., O'Donnell, P., Ollvar, T., Mylor, J., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thoman, D., Tirrell, A., Vassiliev, H., Viel, R., Talamas, J., Tesfaye, S., Theodore, J., Zimmer, A., and Zody, M., Zimmisain, M., Viel, R., Wux, K., Wyman, D., Ye, W. J., Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 01 Jul 13, 2000 this sequence version replaced 91:6705580. Center: Whitehead Institute/ MIT Center for Genome Research Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html * NoTE: This record contains 76 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced
* will be sequenced to completion. In the event that
* will be sequenced to completion. Contact: sequence_submissions@genome.wi.mit.edu the record is updated, the accession number will be preserved.) bp 895 bp in length 862: contig of 862 bp in length 1851 1950: gap of 888 bp in length 1950: gap of 188 bp in length 1951 2817: con+'... of 100 bp contig of 867 bp in length P of 100 bp contig of 871 bp in length contig of 872 bp in length of 100 bp contig of 865 bp in length 12584 12683: gap of 100 bp 12684 13570: contig of 887 bp in length 13571 13570: gap of 100 bp 13671 14560: contig of 890 bp in length 14561 14660: gap of 100 bp 15536: contig of 876 bp in length bp in length of 100 bp contig of 886 bp in length of 100 bp contig of 871 bp in length 7: gap of 100 bp 10614: contig of 877 bp in length 10607: contig of 893 bp in length 11607: contig of 893 bp in length contig of 876 bp in length Center code: WIBR Web site: http://www-seq.wi.mit.edu 100 bp 100 bp contig of 895 contig of 860 Center clone name: 329_H_16 100 Center project name: 3788: con con 11607 6820: gap of 7680: con): gap of 8666: con 11707: gap of 12583: conf 3888: gap of 4760: co 4860: gap of 5725: cor 5825; gap of 6720; col 8766; gap of 9637: co 2917: 7780: 9737: 10714 11608 TITLE JOURNAL

COMMENT

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8616: gap of 100 bp 100 bp 19500: contig of 884 bp in length 20455: contig of 855 bp in length 1555: gap of 100 bp 21441: contig of 886 bp in length 1541: gap of 100 bp 1
15537 15636: gap of 100 bp
15637 16521: contig of 885 bp in length
16522 16621: gap of 100 bp
16622 17518: contig of 897 bp in length
                                                                                                                                       17519 17618: gap of 100 bp 17619 18516: contig of 898 bp in length
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1886 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22518: gap of 100 bp
23376: contig of 858 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76: gap of 100 bp
24342: contig of 866 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of 100 bp 11. contig of 890 bp in length 25. contig of 864 bp in length gap of 100 bp 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29148: contig of 886 bp in length
48: gap of 100 bp
30154: contig of 906 bp in length
54: gap of 100 bp
31124: contig of 870 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 871 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig of 868 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24: gap of 100 bp 32105: contig of 881 bp in length 100 bp 33093: contig of 888 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p of 100 bp contig of 885 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78: gap of 100 bp
34826: contig of 648 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ontig of 845 bp in length contig of 880 bp in length
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1888 bp in length
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48478: contig of 899 bp
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                                                                                                                                                                                                                                                                           19501 19600: gap of
19601 20455: con
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27194:
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29148: cont
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35771: cont
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40673: cont.
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43606: cont.
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37741: conf
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39678: cont
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42631: cont
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47479: con+
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50430: cont
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44387: -
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46994: cont
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16130: cont
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21414: cont
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33770: con'
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41105: con
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72257: conf
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I (bases 1 to 114541)

Burton,J.

Direct Submission

Submitted (06-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Sep 9, 2000 this sequence version replaced gi:9715666.
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rf 899 bp in length
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1881 bp in length
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                  51530: gap of 100 bp 52409: contig of 879 bp in length
                                                                 p of 100 bp contig of 876 bp in length p of 100 bp contig of 891 bp in length
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857 bp in length
  contig of 900 bp in length
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893 bp in length
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68104: contig of 881
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54376: contig of
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55333: contig of
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65168: con+
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27: gap of
67123:
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52510 53385: cont
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60220: cont
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61212: con
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63167: con
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66137: cont
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Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Bly Dye; 100% of reads
Chemistry: Dye-terminator Bly Dye; 100% of reads
Consensus quality: 92792 bases at least Q40
Consensus quality: 99799 bases at least Q20
Insert size: 111641; sum-of-contigs Q20
Insert size: 17321; 12.8% error; agarose-fp
Quality coverage: 1.80x in Q20 bases; sum-of-contigs Quality
Coverage: 2.06x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 2540: contig of 2540 bp in length
2541 2640: gap of 100 bp
2641 4832: contig of 2192 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4932: gap of 100 bp
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10006: contig of 2253 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig of 6024 bp in length
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contig of 6407 bp in length
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                Contact: humquery@sanger.ac.uk
Web site: http://www.sanger.ac.uk
                                                                                                     --- Summary Statistics
                                                                             Center project name: bA477H21
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87060 87159; gap of
87160 94342; conti
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Direct Sylvanor L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Shiren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Bachal, N., Deckely, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaftad, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwar, P., McGurk, A., McKennan, K., McLaughlin, J., Meldrim, J., McTow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W. J., Zimmet, A. and Zody, M. Mheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmet, A. and Zody, M.
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Homo sapiens clone RP11-15N22, WORKING DRAFT SEQUENCE, 29 unordered
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatWasker.html
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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49386. .54379
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142149 159511: conti
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                           Center clone name: 15_N_22
Center clone name: 15_N_22
Center clone name: 15_N_22
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 15473 bases at least Q40
Consensus quality: 153390 bases at least Q30
Consensus quality: 154777 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 168000; agarose-fp
Quality coverage: 3.6 in Q20 bases; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; sum-of-contigs
                                                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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54379: contig of 4994 bp in length
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67094 74249: contig of 7156 bp in length
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83893; contig of 9544 bp in length
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contig of 4512 bp in length
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41124: contig of 4154 bp in length
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15547: contig of 3286 bp in length
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contig of 1258 bp in length
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36870: cont
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60438: cont
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18501: cont
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20423: cont
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9218: cor
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                                                               Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC024315 165858 bp DNA HTG 26-MAY-2000
Homo sapiens clone RP11-26N3, WORKING DRAFT SEQUENCE, 14 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 165858)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-26N3
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Smit, A.F.A. & Green, P. (4996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                         2801 others
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                                                                 Align seg 1/1 to: AC012346 from: 1 to: 159511
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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08-881509-7 x AC012346
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REFERENCE AUTHORS

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* NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                     Sequencing vector: M13: M77815; 100% of reads Sequencing vector: M13: M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 154942 bases at least Q40 Consensus quality: 165960 bases at least Q30 Consensus quality: 165265 bases at least Q30 Insert size: 164000; agarose-fp Insert size: 164558; sum-of-contigs Quality coverage: 4.6 in Q20 bases; sum-of-contigs Quality coverage: 4.6 in Q20 bases; sum-of-contigs
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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88083 110113: contig of 22031 bp in length
110114 110213: gap of 100 bp
110214 133760: contig of 23547 bp in length
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133861 165858: contig of 31998 bp in length.
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54868 70875: contig of 16008 bp in length
70875 70975: gap of 100 bp
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/note="assembly_fragment"
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1. .165858
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18754 27335: cont
                                                                                                                   Center clone name:
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GenBank staff at the National Library of Medicine created this entry [NCBH gibbsq 63879] from the original journal article.
This sequence comes from Figure 4.
Location/Qualifiers

I. 716
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I. 716
/ob_xref="taxon:9606"

I. 716
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1 (Dases 1 to 716)
Griesinger,F., Jansen,B. and Kersey,J.H.

Differentiation in mature T lymphoid leukemia cells is unstable and reversible to myeloid cells, without the involvement of a common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seg_documentation_block: 716 bp DNA PRI 04-MAY-2000 563879 563879 DEFINITION TCR V alpha "T cell receptor variable alpha chain (human, MT-ALL, Genomic Mutant, 716 nt].
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a 34483 c 34023 g 47184 t
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S63879.1 GI:238692
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4.800
90.909
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08-881509-7 x AC024315/rev
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Quality:
Ratio:
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KEYWORDS
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o sapiens chr
o sapiens chr
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                                                                                                                                                                                                                                                                                                       Tumor-infiltrating lymphocytes recognizing spontaneously arising renal cell carcinomas express T cell receptors characteristic of
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                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutherla; Primates; Catarrhin1; Hominidae; Homo. 1 (bases 1 to 1318) Jantzer, P. U. and Schendel, D. J.
 i AC027717 HOMO 5
i AC010217 HOMO 5
i AC010272 HOMO 5
i AC011940 HOMO 5
                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (11-JW-1996) P. Jantzer, Institute for Immunology,
Goethestr. 31, D- 80336 Munich, FRG
Goethestr. 31, D- E00316 Munich, FRG
                                                                                                                                08-JAN-1997
                                                                                                                                             H. sapiens mRNA for rearranged TCR junctional sequences
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        151974
154690
155306
169075
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          5.0e+03
5.1e+03
5.1e+03
5.5e+03
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A93131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                        mRNA
             93.05
92.93
92.90
92.30
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LOCUS A93131
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08-881509-8 x HSTCRJUNC
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                                                                                          seq_name: gb_pr7:HSTCRJUNC
                                                                                                                            seq_documentation_block:
LOCUS
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               gb_htg13:AC027717
gb_htg3:AC010217
gb_htg3:AC010272
                                                                gb_htg4:AC011940
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35112 i Ac001649 Drosophila melanogas
69017 i AL031732 Human DNA sequence
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i ACO193806 Mus musculus clone
i ACO16554 Homo sapiens chrome
i ACO04999 Homo sapiens PAC Cl
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51 : AF043886 Homo sapiens patient CS
48 : U27254 Human isolate M30 T-cell
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),0128 1318 : X98410 H.sapiens mRNA for rear
),0107 39 : A93131 Sequence 5 from Patent EF
),0107 98 : S6910 TCR V alpha-T-cell recept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1341 | A93127 Sequence 1 from Patent 87 | L42801 Homo Sapiens (clone NSI-157437 | AC021669 Homo Sapiens chrome 172581 | AC009319 Homo Sapiens 3 BAC 175814 | AC048347 Homo Sapiens chrome 258550 | AC040378 Homo Sapiens chrome 258550 | AC040378 Homo Sapiens chrome 258550 | AC010758 Homo Sapiens Chrome ACO405158 Ho
                                                                                                                                             About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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                                  OM of: 08-881509-8 to: GenEmbl:* out_format : pfs
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4.3e+03
4.9e+03
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.0e+03
.1e+03
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1194.90
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Database sequences: 1118133
Database length: -1736092196
Search time (sec): 3669.890000
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                                                                       Date: Apr 1, 2001 4:45 AM
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                                                                                                                                                    Command line parameters:
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gb_htg6:AC016554
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gb_pr6:HSA235208
gb_htg8:AC021520
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gb_htg14: AC055413
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gb_htg14:AC048347
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em_in:DMAC01649
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gb_htg8:AC021669
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gb_pr7:HSU40776
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gb_pat1:A93131
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KEYWORDS

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conflict with the conceptual translation"
                                                                                                                                                                                                                                    4.750 Gaps: 0
85.714 Percent Identity: 78.571
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                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 78.571
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                                                                                                                                              28 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treells specific for kidney carcinoma
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
                                                                                                                                                                                                                             Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1 from Patent EP0816496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAB69529.1"
/db_xref="GI:6741517"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unidentified"
                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: 'S69140 from: 1 to: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: A93127 from: 1 to: 1341
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                                                                                                                                              20 g
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Schendel, D.J.
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a 365 c
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unclassified.
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08-881509-8 x S69140
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Ratio:
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 98)
Mohapatra, S.S., Mohapatra, S., Yang, M., Ansari, A.A., Parronchi, P., Maggi, E. and Romanani, S.
Molecular basis of cross-reactivity among allergen-specific human T Immunology 81 (1), 15-20 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION TOR V alpha=T-cell receptor alpha-chain (allergen-specific) (human grass sensitive individual VI 19, peripheral blood, mRNA Partial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="TcR v alpha"
/note="This sequence comes from Fig. 3b; Protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenBank staff at the National Library of Medicine created this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry [NCBI glbbsq 144562] from the original journal article. This sequence comes from Fig. 3a.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human peripheral blood grass-sensitive individual VI 19.
                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 84.615
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                                                                                                                                                                                                            /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CysLeuAlaLeuAlaGlySerAlaArgGlnLeuThrPhe 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-cells specific for kidney carcinoma
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
Location/Qualifiers
                                                                                                                                                                                                                                           /protein_id="CAB69531.1"
/db_xref="G1:6741521"
/translation="CLVLSGSARQLTF"
                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                              /organism="unidentífied"
                                                                                                                                                                             /db_xref="taxon:32644"
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/db_xref="taxon:9606"
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                                              1 (bases 1 to 39)
Schendel, D. J.
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Percent Similarity: 100.000
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unidentified.
unidentified
                                  unclassified
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LOCUS S69140
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KEYWORDS
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//Translation="MRQVARVIVELTLSTLSLAKTTQPISMDSYEGGEVNITCSHNNI
ATNDYITWYQQPPSQGPRFIIQGYKTKVTNRVASLFIPADRKSSTLSLPRVSLSDRAV
YYCLVGGSARQLIFGSGTQLTVLPDIONPDPAVYQLRDSKSSDKSVCLFTDFDSQTNV
SQSKDSDVYITDKTVLDMRSMDFKSNSAVAMSNKSDFACANAFNNSIIPEDFFFPSPF
SSCDVKLVEKSFFTDTNLNFQNLSVLGFRILLLKVAGFNLLMTLRLMSS"
/codon_start=1
/exception="Protein longer than coding region shown;
// mismatch(12[E-56]).
// protein_id="AAB30244.1"
// Ab_xref="G1:545974"
// translation="DSATYFCAALPESARQLTFGSGTQLTVLPDIQN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JAN-2000
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ORGANISM

KEYWORDS

VERSION SOURCE REFERENCE

DEFINITION

ACCESSION

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Submitted (19-Jan-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasKer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Context: sequence_submissions@genome.wi.mit.edu
Context project Information
Center clone name: 129_F_9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 15/437; sum-of-contigs
Insert size: 15/437; sum-of-contigs
Quality coverage: 4.9 in Q20 bases; sum-of-contigs
Quality coverage: 4.4 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1296: contig of 1296 bp in length
gap of unknown length
3134: contig of 1838 bp in length
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1 (bases 1 to 157437)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone RP11-129F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ength
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Web site: http://www-seq.wi.mit.edu
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gap of unknown
49008: contig of 9922
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gap of unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zimmer, A. and Zody, M. Direct Submission
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                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                           JOURNAL
REFERENCE
                   REFERENCE
                                         AUTHORS
                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clonal expansion of myelin basic protein-reactive T cells in patients with multiple sclerosis: restricted T cell receptor V gene rearrangements and CDR3 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vandevyver, C., Mertens, N., van den Elsen, P., Medaer, R., Raus, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC021669 157437 bp DNA HTG 19-JAN-2000 HOM Sapiens chromosome 18 clone RP11-129F9 map 18, WORKING DRAFT SEQUENCE, 15 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 87)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (19. 75), partial TCRCA (76. .87)" //Obs.ref="GDB:G00-120-404" //product="T coll
                                                                                                                                                                                            Homo sapiens (clone NSI-F4) T cell receptor alpha chain (TCRA) IA2801
                                                                                                                                                                                 07-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="T cell receptor alpha chain"
/protein_id="AaA80964.1"
/db_xref="G1:853663"
/translation="FECAEASGSARQITFGSGTQLTVLPDIQK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 64.286
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                        T cell receptor alpha.
Homo sapiens (clone: NS1-F4) cDNA to mRNA.
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="NS1-F4"
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LOCUS AC021669 157437 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="TCRA"
                                                                                                                                                                                                                                                                                                L42801.1 GI:853662
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08-881509-8 x HUMTCRACG
                                                                                                            seq_name: gb_pr8:HUMTCRACG
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LOCUS
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Ratio:
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BASE COUNT

gene

CDS

MEDLINE

FEATURES

JOURNAL

TITLE

DEFINITION

ACCESSION KEYWORDS

VERSION

ORGANISM

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 172581)

Muzny,D.M., Adams,C. Bailey,M., Barbaria,J., Blankenburg,K., Buoke,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C., Burket,C., Burrows,J., Carter,M., Chacko,J., Chen,Z., Cox,C., David,R., Delgado,O., Deshazo,D., Ding,T., Domah-Rashid,N., Fordan-Tansey,J., Fernaddez,C., Ferraguto,D., Fordan-Tansey,J., Fernaddez,C., Ferraguto,D., Gorrell,L.L., Guevara,W., Harris,K., He,X., Hernandez,J., Jackson,L., Jackson,L., Jackson,L., Jackson,L., Jackson,L., Lia,Y., Jones,M., Holly,S., Kondejewski,N., Kong,Y., Kovar,C., Leal,B., Liz,Z., Lichtarge,O., Liu,J., Liu,M., Logan,O., Mel,G., Moore,S., Moorish,T., Morgan,M., Martinez,C., McLeod,M.P., Nelson,A., Nguyen,R., Nguyen,R., Nguyen,R., Nguyen,R., Nguyen,R., Nguyen,R., Scherer,S., Shah,E., Shen,H., Vasquez,L., Vinson,R., Vo,Q., Wahbah,M., Wallington,S., Weinstock,I.R., Williamson,A., Wolley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Naylor,S., Nasla,C., Weinstock,I.R., Williamson,A., Worley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Naylor,S., Nelson,R., Weinstock,I.R., Williamson,A., Worley,K., Wren,J., Wrensford,G., Yu,W., Zhou,X., Naylor,S., Callabba,R., Weilson,R., Naylor,S., Callabba,R., Weilson,R., Weilson
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Homo sapiens 3 BAC RPI1-297K7 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
gap of unknown length contig of 13479 bp in length of unknown length 74733: contig of 12246 bp in length gap of unknown length gap of unknown length gap of unknown length 104301: contig of 15027 bp in length
                                                                                                                                                                                                                                                                                                                  contig of 18736 bp in length
gap of unknown length
contig of 34400 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_"RP11-129F9"
/clone_lib="RPCI-11 Human Male BAC"
39877 a 39144 c 38679 g 39736 t 1 c
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Percent Identity: 64.286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="18"
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Percent Similarity: 85.714
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08-881509-8 x AC021669/rev
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LOCUS AC009319 13
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones overlapping clones are noted at the beginning and end of the
                                                                                           Submitted (16-AŭG-1999) Human Genome Sequencing Center, Department Of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 172581)
                                                                                                                                                                                                                                                   Direct Submission
Submitted (28-JUL-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 172581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission Submission Submitted (25-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 28, 2000 this sequence version replaced gi:9438826. INFORMATION: http://www.hgsc.bcm.tmc.edu/or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (12-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 172581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             annotation as Low Coverage.
      (bases 1 to 172581)
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2 (bases 1 to 172 Worley, K.C.
Direct Submission
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/note="Unigene cluster similar to: SEG_HSLPP Human lipoma

/rpt_family="(TATATG)n" 938. .6929

misc_feature

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178443. 15191
15195. 15216
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15196. 15516
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/rpt_family=malich
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/rpt_family=malich
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15652. .15996
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/ur-HF-BNO-alf-f-08-0-UI.rl Homo sapiens CDNA: AW503943"
complement(16516. .17018)
/note="Region Similar to: Hs#S1739629
UI-H-BWO-ajp-d-04-0-UI.sl Homo sapiens CDNA: AW298030"
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complement(9379. .9851)
/note="Region similar to: Hs#S1816152 hd44d11.x1 Homo sapiens cDNA: AW511222"
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complement(19962. .20058)
/rpt_family="L2"
complement(21429. .21723)
partner (LPP) gene"
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/rpt_family="AluSx"
25419. .25705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="L1ME"
complement(25706. .25981)
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complement(11625. .11879)
/rpt_family="Alur"
12336. .12639
                                                                                    8121. .8205
/rpt_family="CT-rich"
complement(8904. .9214)
/rpt_family="Alux"
                                                                                                                                                                  8933. .9073
/function="Low Coverage"
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/rpt_family="AluJo"
7630. .7677
/rpt_family="A-rich"
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/rpt_family="AluSq"
23446. .23726
/rpt_family="AluSx"
23767. .23831
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21913. 21989
/rpt_family="(TA)n"
21990. /rpt_family="LiM4"
22720. 22894
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23175. .23407
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24495, 24865
/rpt_family="L1"
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21804. .21912
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla: Eutheria; Primates; Catarrini; Hominidae; Homo.

1 (bases 1 to 175814)

RS Muzny, D.M., Adams, C., Balley, M., Barbaria, J., Blankenburg, K.,

Bodofta, B., Bouck, J., Bowie, S., Brooks, A., Bunac, C.,

Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox. C.,

David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,

Buyan-Roccha, S., Durbin, K.J., Fernandez, C., Ferraguto, D.,

Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J.H., Gorrell, L.L.,

Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M.,

Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,

Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R.J., Lu, J.,

Lucier, R., Martin, R., Martinez, C., McLeed, M.P., Mel, G., Morgan, M.,

Morris, S., Nash, S., Nelson, A., Nuguen, R., Nuguen, N., Nuguen, S.,

Guiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S.,

Shah, E., Shen, H., Simon, M., Samuel, S., Say, J., Scherer, S.,

Matlington, S., Weinstock, G., Weinstock, I.R., Williamson, A.,

Watlington, S., Weinstock, G., Weinstock, I.R., Williamson, A.,

Direct Submission

AL Uppublished

La Chases 1 to 175814)
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LOCUS ACO48347 175814 bp DNA HTG 01-SEP-2000
DEFINITION Homo sapiens chromosome 12 clone RP11-367G12, WORKING DRAFT
SEQUENCE, 19 unordered pieces.
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85.714 Percent Identity: 57.143
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                                                                                                                                                                                             /rpt_family="MER67B"
31541. 31633
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/rpt_family="MER20"
31990. 32040
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32348. 32369
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28306. .28967
                                                                       26602. .26657
/rpt_family="AT_rich"
complement(26752. .27
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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08-881509-8 x AC009319
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AUTHORS TITLE JOURNAL

COMMENT

Location/Qualifiers

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* NOTE: This is a 'working draft' sequence. It currently
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NOTE: This is a "working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                     Sequencing vector: M13: L08821
Sequencing vector: M13: L08821
Sequencing vector: M13: L08821
Chemistry: Dye-primer Bodipy: 28 of reads
Chemistry: Dye-terminator B14 Dye: 72% of reads
Assembly program: Phrap; version 0.99329
Consenus quality: 156908 bases at least 040
Consensus quality: 170374 bases at least 020
Consensus quality: 170374 bases at least 020
Estimated insert size: 170493; sum-of-contigs estimation
Quality coverage: 0x in 020 bases; sum-of-contigs estimation
Quality coverage: 3.6x in 020 bases; sum-of-contigs estimation
Worley, K.C.
Direct Submission
Submitted (14-APR-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Ravlor Plaza, Houston, TX 77030, USA
Ravlor Plaza, Houston, TX 77030, USA
                                                                               contig of 15195 bp in length
gap of unknown length
contig of 15080 bp in length
app of unknown length
contig of 10474 bp in length
gap of unknown length
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gap of unknown length
contig of 21001 bp in length
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29911: gap of unknown length
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gap of unknown length
contig of 10042 bp in length
gap of unknown length
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of 1734 bp in length.
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                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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gap of unknown 1
contig of 3143 b
gap of unknown 1
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gap of unknown
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gap of unknown
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                                                                                                                                                                                                                   Center project Information
Center project name: HATW
Center clone name: RP11-367612
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Particle (Controller)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balten, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguelavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Costle, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vaszliiev, H., Vo, A., Wheeler, J., Wu, X., Direct Submission

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 258550)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu ------ Project Information Center project name: L1428
                                                                                                                       1828 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-1B18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR Web site: http://www-seq.wi.mit.edu
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-367612"
50954 a 35383 c 35133 g 52516 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AC048347 from: 1 to: 175814
                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone name: 1_B_18
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                                                                                                                                                                                                                                                                                                   Ratio: 4.083
Percent Similarity: 85.714
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                                                                                                                                                                                                                                                                        49.00
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08-881509-8 x AC048347
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Ratio:
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                                                                                                                                                                                                                                               alignment_scores:
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consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                      13494 13593; gap of 100 bp 13594 20146: contig of 6553 bp in length 20147 20246; gap of 100 bp 20247 31323; contig of 11077 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                           p of 100 bp contig of 12639 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84039 84138; gap of 100 bp 84139 96604; contig of 12466 bp in length 96705 104482; contig of 7778 bp in length 10483 104582; contig of 7778 bp in length 128830 128929; gap of 100 bp 100 bp 128830 128929; gap of 100 bp 128930; contig of 16990 bp in length 128830 1245919; contig of 16990 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145920 146019; gap of 100 bp 176142 176141; contig of 30122 bp in length 176142 176241; gap of 100 bp 100 bp 176242 199362; contig of 14121 bp in length
                                                                                                                                                                             2184 2283: gap of 100 bp 2284 5870: contig of 3587 bp in length 5871 5970: gap of 100 bp 5971 13493: contig of 7523 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190363 190462: gap of 100 bp 190463 208674: contlg of 18212 bp in length 208675 208774: gap of 100 bp 100 bp 208775 228999: contlg of 20225 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229000 229099: gap of 100 bp
229100 258550: contig of 29451 bp in length.
Location/Qualifiers
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                                                                                                                                                          2183: contig of 2183 bp in length
                                                                                                                                                                                                                                                                                                                                                                     contig of 7315 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           77: gap of 100 bp 59570: contig of 7993 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70: gap of 100 bp 67050: contig of 7380 bp in length 50: gap of 100 bp 74878: contig of 7728 bp in length
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84038: contig of 9060 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 145471 TTCTGCCTTCCTCTGGCGGGGGGGGGGGGGGGGGGAATGACATTT 145512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-11 Human Male BAC"
71311 a 57160 c 56642 g 69733 t 3704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                31423: gap of
38738: cont
                                                                                                                                                                                                                                                                                                                                                                                                             38838: gap of
51477: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59670: gap of
67050: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67150; gap of
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                                                                                                                                       be preserved.
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08-881509-8 x AC010758
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Submitted (15-OCT-1998) Cross S.M., Queensland Institute of Medical Research, The Bancroft Centre, 300 Herston Road, Brisbane, AUSTRALIA 4029
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
  HSA235208 42 bp mRNA PRI 12-MAR-1999 Homo sapiens mRNA for T cell receptor alpha chain V-J junctional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 73806)

Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-329H16
                                                                                                                                                                                                                                                                                                                                                                                                   Crossreactive recognition of viral, self, and bacterial peptide ligands by human class I-restricted cytotoxic T lymphocyte clonotypes: implications for molecular mimicry in autoimmune
                                                                                                       T cell receptor; T cell receptor alpha chain; variable region.
                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 42)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION Homo sapiens chromosome 17 clone RP11-329H16 map 17, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 42)
Misko,I.S., Gross,S.M., Khanna,R., Elliott,S.L., Schmidt,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 96 (5), 2279-2284 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="blood"
/cell_type="cytotoxic T lymphocyte"
| (cell_line="SP1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity: 92.308 Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/haplotype="A1, A2, B8, B45, Bw6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CysLeuAlaLeuAlaGlySerAlaArgGlnLeuThrPhe 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGCGCTGTTTTTTCTGGTTCTGCAAGGCAACTGACCTTT 39
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                                             (TCRAV7AJ16S3).
                                                                                   AJ235208.1 GI:3851223
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LOCUS AC021520 73806 bp
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6
                                                                                                                                                                                                                                                     Direct Submission
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                                                                                                                                                    Homo sapiens
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08-881509-8 x HSA235208
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HSA235208
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                                                                   AJ235208
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                                               region
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                    DEFINITION
                                                                                                                                                ORGANISM
                                                            ACCESSION
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                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                       KEYWORDS
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REFERENCE
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TITLE JOURNAL COMMENT

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32 42731: gap of 100 bp 32 43506: contig of 875 bp in length 37 45139: contig of 835 bp in length 37 45139: contig of 833 bp in length 40 44539: gap of 100 bp 40 45524: contig of 885 bp in length 25 45524: contig of 888 bp in length 455212: contig of 888 bp in length 35 45512: contig of 888 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28263 29148; contrig of 906 bp in length 29149 30154; contrig of 906 bp in length 30155 30254; gap of 100 bp 30255 31124; contrig of 870 bp in length 3125 31205; contrig of 881 bp in length 3206 32205; gap of 100 bp 3206 33093; contrig of 888 bp in length 33094 33193; gap of 100 bp 3206 33093; contrig of 888 bp in length 34078; contrig of 885 bp in length 34078; contrig of 648 bp in length 34179; 34926; gap of 100 bp 34076; contrig of 648 bp in length 3477 34926; gap of 100 bp
                                                                                                                                                                                                                                                                                                              2 2055; gap of 5 2055; gap of 6 2055; gap of 6 21441: contig of 886 bp in length 42 21541: gap of 100 bp 22418: contig of 877 bp in length 19 2376; contig of 878 bp in length 19 2376; contig of 878 bp in length 19 2442: contig of 866 bp in length 43 2442: gap of 100 bp 100 bp 143 2523; contig of 866 bp in length 43 2523; contig of 90 bp in length 19 2523; contig of 90 bp in 19 2523; contig of 90 bp in length 19 2523; contig of 90 bp in length 19 2523; contig of 90 bp in length 19 2523; contig of 90 bp
15537 15636: gap of 100 bp
15637 15621: contig of 885 bp in length
16522 16621: gap of 100 bp
16522 17518: contig of 897 bp in length
17519 17618: gap of 100 bp
17519 18515: contig of 898 bp in length
18517 18616: gap of 100 bp
18617 19500: contig of 884 bp in length
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48478: contig of 899 bp in length
778: gap of 100 bp
49448: contig of 870 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p of 100 bp
contig of 882 bp in length
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40673: contig of 895 bp in length
773: gap of 100 bp
41671: contig of 898 bp in length
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42631: contig of 860 bp in length
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38806 39678: contig of 873 bp in length
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34927 35771: contig of 845 bp in length
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35872 36751: contig of 880 bp in length
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27294: gap of 100 bp
28162: contig of 868 bp in length
28262: gap of 100 bp
29148: contig of 886 bp in length
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49448: cont
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                   Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreitar, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Morman, J., Marduis, N., McEwan, P., McGurk, A., McKernan, K., Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Severy, P., Spencer, B., Stanger-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tasfaye, S., Theodore, J., Stojanovic, N., Subramanian, A., Talamas, J., Tasfaye, S., Theodore, J., Tirrell, A., Vassiliew, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Tirrell, A., Vassiliew, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Limmer, A. and Zody, M.

Direct Submission

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Center

Center: Whitehead Institute/ MIT Center for Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu ------ project Information Center project name: L5499
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963 1850: contig of 888 bp in length
1851 1950: gap of 100 bp
1851 2817: contig of 867 bp in length
1951 2817: contig of 867 bp in length
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14660: gap of 100 bp
15536: contig of 876 bp in length
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2918 3788: contig of 871 bp in length
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4760: contig of 872 bp in length
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6720: contig of 895 bp in length
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f 886 bp in length
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13570: contig of 887 bp in length
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of 871 bp in length
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8666: con
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9637: co
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5725: co
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7680: co
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 114541)
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Burton, J.

Burton, J.

Burton, J.

Submitsed (06-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Sep 9, 2000 this sequence version replaced g1:9715666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens chromosome 1 clone RP11-477H21, *** SEQUENCING IN PROGRESS ***, 30 unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 61320: gap of 100 bp 113 61312: contig of 892 bp in length 13 61312: gap of 100 bp 
                          51530: gap of 100 bp 52409: contig of 879 bp in length 52509: gap of 100 bp 53385: contig of 876 bp in length 53485: gap of 100 bp
51430: contig of 900 bp in length
                                                                                                                                                                                                                                                                                                   contig of 891 bp in length
                                                                                                                                                                                                                                                                                                                                        54476: gap of 100 bp 55333: contig of 857 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                  op of 100 bp
contig of 856 bp in length
p of 100 bp
contig of 893 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57382: gap of 100 bp 58278: contig of 896 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78: gap of 100 bp 59254: contig of 876 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of 100 bp
contig of 866 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66137: contig of 869 bp in length 100 bp 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bp in length
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65168: contig of 899 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
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57282.
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56289:
                                                                                                                                                                                                                                                   85: gap of 54376: cont
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60220: cont
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66137: cont
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HTG: HTGS_PHASE1.
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08-881509-8 x AC021520
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----- Genome Center

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Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Gequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 92902 bases at least 040
Consensus quality: 99799 bases at least 030
Consensus quality: 104556 bases at least 020
Insert size: 111641; sum-of-contigs
Insert size: 17321; 12.8% error; agarose-fp
Quality coverage: 1.80x in 020 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2540: contig of 2540 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7654 7753: gap of 100 bp 7754 10006: cont19 of 2253 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 100 bp
contig of 2192 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 100 bp contig of 2721 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10007 10106: gap of 100 bp
10107 16130: contig of 6024 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30: gap of 100 bp
21414: contig of 5184 bp in length
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23969: contig of 2455 bp in length
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27263: contig of 3194 bp in length
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72257: contig of 2775 bp in length
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81052: contig of 5165 bp in length
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                                                  Web site: http://www.sanger.ac.uk
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33770
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46994: cont
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56148: con+
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(4: gap of
66987:
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75787: ....
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33871 37774; cont
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51529 53697: cont
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2641 4832: co
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Sanger Centre
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                Center code: SC
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102726 102825: gap of 100 bp 102826 104971: contig of 2146 bp in length 104972 105071: gap of 100 bp 105072 112223: contig of 7152 bp in length 112224 112323: gap of 100 bp 112324 114541: contig of 2218 bp in length. Location/Qualifiers
94343 94442: gap of 100 bp
94443 97259: contig of 2817 bp in length
97260 97359: gap of 100 bp
97360 993869: contig of 2510 bp in length
                                                                99870 99969; gap of 100 bp 102725; contig of 2756 bp in length
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41206. .44387
/note="assembly_fragment:00231"
44488. .46994
/note="assembly_fragment:00479"
47095. .51428
/note="assembly_fragment:00511"
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/note="assembly_fragment:00812"
72358. .75787
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fragment_chain:1"
7754. 10006
/note="assembly_fragment:01149
fragment_chain:1"
10107 16130
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/note="assembly_fragment:00560"
53798. .56148
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/note="assembly_fragment:00618"
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67088, .69387
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2641. 4832
/note="assembly_fragment:00907
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4933. 7653
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RS Birren, B., Linchon, L., Buckerly, R., Boquslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boquslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boquslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Groke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Funke, R., Gage, D., FitzHugh, M., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J., Gardyna, S., Grant, G., Kann, L., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McUawan, P., McGurk, A., McKeran, K., McLaughlin, J., Meldrim, J., McUawan, P., McGurk, A., McMann, K., Connor, T., O'Donnell, P., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Pirk, A., Chan, J., Ye, W., J., Zimmer, A. and Zody, M.
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HOMO sapiens clone RP11-15N22, WORKING DRAFT SEQUENCE, 29 unordered
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Submitted (15-00r-1999) Whitehead Institute/MIT Center for Genome Submitted (25-00r-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 22, 2000 this sequence version replaced 91:7657752.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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1 (bases 1 to 159511)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome, clone RP11-15N22
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HTG: HTGS_PHASE1; HTGS_DRAFT.
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...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                 Center project name: 13497

Center clone name: 15_N_22

Center clone name: 15_N_22

Center clone name: 15_N_22

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 155390 bases at least Q40

Consensus quality: 154377 bases at least Q30

Insert size: 166000; agarose-fp

Insert size: 156711; sum-of-contigs
Quality coverage: 3.6 in Q20 bases; agarose-fp

Quality coverage: 3.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                     Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1018: contig of 1018 bp in length
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contig of 1776 bp in length
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28977: contig of 1892 bp in length
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41124: contig of 4154 bp in length
41224: gap of 100 bp
45905: contig of 4681 bp in length
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83893; contig of 9544 bp in length
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54480 60438: contig of 5959 bp in length
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                                                   Web site: http://www-seq.wi.mit.edu
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36870: con
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4272: co
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4373 5630; cor
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102848 102347: gap of 100 bp 102948 116070: contig of 13123 bp in length 116171 128705: contig of 13123 bp in length 128706 128805: gap of 100 bp 128806: 142048: gap of 100 bp 128804: gap of 100 bp 128804: gap of 100 bp 128804: gap of 100 bp 12849: gap of 100 b
993: gap of 100 bp
92494: contig of 8901 bp in length
5349 app of 100 bp
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2245. .4272
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I. Unton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Baidwin, J., Bardan, N., Bada, F., Boguslavkiy, L., Anderson, S., Baldwin, J., Bardan, N., Bada, F., Boguslavkiy, L., Anderson, S., Baldwin, J., Burkett, G., Campoplano, A., Costele, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Dearellano, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Perrestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Grant, G., Hados, B., Heaford, A., Horton, L., Karatas, A., Howland, J.C., Illev, I., Johnson, W., Johnson, Y., Lehoczky, J., Levine, R., Lieb, J., Largocque, K., Lehoczky, J., Levine, R., Lieb, J., Langocque, K., Lehoczky, J., Levine, R., Lieb, J., Langocque, K., McChena, P., Mardonald, P., Marquis, N., McCarthy, M., McCarran, K., McRornan, R., O'Reall, D., Oilvar, T.M., Norman, C.H., O'Connor, T., O'Connel, P., O'Reall, D., Oilvar, T.M., Severy, P., Spencer, B., Stange-Thomann, N., Stolavor, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolavor, J., Tirrell, A., Tiglilio, J., Yeskiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zalnoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC024\overline{3}15 165858 bp DNA HTG 26-MAY-2000 HOMO sapiens clone RP11-26N3, WORKING DRAFT SEQUENCE, 14 unordered
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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1 (bases 1 to 165858)
Birran, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, Conne RP11-26N3
Unpublished
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50583 a 29248 c 29765 g 47114 t
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Percent Similarity: 85.714
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LOCUS AC024315 16
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KEYWORDS

VERSION SOURCE TITLE

COMMENT

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NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                       Center Colone name: 26_N_3

Center Colone name: 26_N_3

Sequencing vector: M13; M778125; 100% of reads

Sequencing vector: M13; M778125; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 154942 bases at least Q40

Consensus quality: 162505 bases at least Q20

Consensus quality: 162505 bases at least Q20

Insert size: 164000; agarose-fp

Insert size: 164568; sum-of-cortigs

Quality coverage: 4.6 in Q20 bases; sum-of-contigs

Quality coverage: 4.6 in Q20 bases; sum-of-contigs
                   Contact: sequence_submissions@genome.wi.mit.edu
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110214 133760: contig of 23547 bp in length
133761 133860: gap of 100 bp
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54868 70875; contig of 16008 bp in length
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88083 110113: contig of 22031 bp in length
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2629 4506: contig of 1878 bp in length
4507 4606: gap of 100 bp
6447: contig of 1841 bp in length
6448 6547: gap of 100 bp
6548 11790: contig of 5243 bp in length
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contig of 1154 bp in length
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Web site: http://www-seq.wi.mit.edu
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18653: cont
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1375 2528: con
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ thases 1 to 716]
Griesinger, F., Jansen, B. and Kersey, J.H.

Differentiation in mature T lymphoid leukemia cells is unstable and reversible to myeloid cells, without the involvement of a common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS S63879 716 bp DNA PRI 04-MAY-2000
DEFINITION TCR V alpha -T cell receptor variable alpha chain (human, MT-ALL,
Genomic Mutant, 716 nt].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"This sequence comes from Figure 4; conceptual translation presented here differs from translation in publication."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 63879] from the original journal article. This sequence comes from Figure 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="T cell receptor variable alpha chain"
                                                                                                                                                                                                                 misc_feature /note="assembly_fragment"

misc_feature /note="assembly_fragment"

misc_feature /note="assembly_fragment"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity: 90.909 Percent Identity: 90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Immunol. 147 (10), 3336-3341 (1991)
92043697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
41799. 54767
/note="assembly_fragment"
54868. 70875
/note="assembly_fragment"
70976. 87982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                         11891, .18653
/note="assembly_fragment"
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/note="TCR V&agr"
join(58. .109,340. .>716)
/gene="TCR V alpha"
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LOCUS S63879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_pr8:S63879
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TITLE
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MEDLINE
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SOURCE
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Sun Apr 1 08:50:48 2001

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| AF058079 HTLV-2 isolate FOR2
| AF058080 HTLV-2 isolate FOR3
| AF058081 HTLV-2 isolate Pl e
| AF058082 HTLV-2 isolate Pl e
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J gene; junction; T cell receptor; TCR junctional sequence; V gene.
human.
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329 c 352 g 344 t 87 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Vertebrata, Mammalia, Eutheria, Primates: Catarrhini, Hominidae; Homo.
1 (basea 1 to 1318)
Jantzer, P. U. and Schendel, D. J.
Tumor-infiltrating lymphocytes recognizing spontaneously arising renal cell carcinomas express T cell receptors characteristic of secondary immune response
                                                                                                                                                                                                                                                                                                                                                                                                        08-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (11-JUN-1996) P. Jantzer, Institute for Immunology, Goethestr. 31, D- 80336 Munich, FRG Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION H. Sapiens mRNA for rearranged TCR junctional sequences.
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Gaps: 0
Percent Identity: 100.000
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/protein_id="CAA67057.1"
/db_xref="GI:1770561"
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/isolate="patients 22 and 26"
/db_xref="taxon:9606"
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123.77
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Jantzer, P.
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Percent Similarity: 100.000
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08-881509-9 x HSTCRJUNC
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                                                      9b_vil:AF058079
9b_vil:AF058080
9b_vil:AF058081
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ACCESSION
VERSION
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KEYWORDS
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! X80241 Human T-cell leukemia vi
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                                                                                                                                                          About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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OM of: 08-881509-9 to: GenEmbl:* out_format : pfs
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0.0386
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4.1e+03
6.5e+03
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Database: GenEmbl:*
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9b_pr8;S69140
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gb_htg4:AC013484
gb_pr7:H0AC002299
gb_htg20:AL160052
gb_pat1:A93133
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9b_htg22:AL360083
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9b_in3:PHE133553
9b_pl3:SCYOR029W
9b_pl3:HVU56406
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gb_vi2:HTLVIIGP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
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                               BASE COUNT
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                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clonal expansion of myelin basic protein-reactive T cells in patients with multiple sclerosis: restricted T cell receptor V gene rearrangements and CDR3 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vandevyver, C., Mertens, N., van den Elsen, P., Medaer, R., Raus, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / note="partial TCRVA (1. .15), TCRNA (16. .18), TCRJA (19. .75), partial TCRCA (76. .87)" (19. .75), partial TCRCA (76. .87)" (40. xref="60Bs:G00-120-404" // product="T cell receptor alpha chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (clone NSI-F4) T cell receptor alpha chain (TCRA) L42801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-NOV-1995
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                                                                                                                                                                                                                                 /note="unnamed protein product"
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                                                                                        T-cells specific for kidney carcinoma
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="G1:6741521"
                                                                                                                                                                               /organism="unidentified"
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                                          unclassified.
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                                                                               Schendel, D.J.
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: Sw.; SWISSPROT: FT: TREMBL: Wp:, WORMPEP; Information to the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromsome 20, constructed, by the Sanger Centre Chromosome 20 http://www.sanger.ac.uk/HGP/Chr20

http://www.sanger.ac.uk/HGP/Chr20

http://www.sanger.ac.uk/HGP/Chr20

park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                together with a note of the overlapping clone name. Note that the together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RRP1-65K20 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP5-1167H4 is at 20504 in this sequence.
The true right end of clone RP1-380D15 is at 100 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL359534 20603 bp DNA PRI 07-SEP-2000 Human DNA sequence from clone RPII-65K20 on chromosome 20 Contains part of a gene for a novel protein similar to vacuolar AFPase isoform VA68. Contains ESTs, STSs and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryoft; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 20603)
/protein_id="aaa80964.1"
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/translation="rFCAEASGSARQLTFGSGTQLTVLPDIOK"
                                                                                                                                                                                                                                                                          Length: 14
Gaps: 0
Percent Identity: 71.429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 TITTGTGCAGAGGCCTCTGGTTCTGCAAGGCAACTGACCTTT 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: HUMTCRACG from: 1 to: 87
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HTG; ATPase.
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Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                              /note="match: cDNAs: Em:AF113129
match: ESTs: Em:N74518 Em:AA418630 Em:R43762 Em:AI797879
Em:AM658428 Em:AI457682 Em:AI03751 Em:AI669434 Em:H23200
Em:H18658 Em:AA576047 Em:AI554929 Em:AA244669 Em:AI142863
Em:AI243726 Em:AIZ72715 Em:AA836368 Em:AI37906 Em:D19704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/product="bA65K20.1 (novel protein similar to vacuolar
APpase isoform vA68)"
complement(join(1450. .1559,1658. .1808))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5504. .5637
/note="LiMBB repeat: matches 5693. .5828 of consensus"
/note="LiMBS repeat: matches 4906. .6168 of consensus"
/note="LiMBB repeat: matches 5821. .6171 of consensus"
/note="LiMBB repeat: matches 5821. .6171 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1561. .1658
/note="149 copies 2 mer ca 76% conserved"
1844. .2310
/note="iipA3 repeat: matches 5680. .6146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8178. 9258
2704c="Lipba repeat: matches -1549. .-412 of consensus"
2746. 10818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7883. . 18189
/note="1.1818 repeat: matches 5979. .6297 of consensus"
8178. .9258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hote "LIPBa repeat: matches -279, .1272 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14024. 14063
/note="20 copies 2 mer at 80% conserved"
14092. 14463
/note="L1PB1 repeat: matches 5783. 6155 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3411. .3515
/note="LIM1 repeat: matches 5536. .5642 of consensus"
                                                                                                                                                                                                                                                         /note="L2 repeat: matches 2320. .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2313. .2356
/note="12 copies 2 mer aa 77% conserved"
2886. .3012
/note="FLAM_C repeat: matches 1. .123 of consensus"
                                                                                                                                                                                                                                                                                            /note="L2 repeat: matches 1840. .2015 of consensus"
complement(1450)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7702. .7882
/note="L2_repeat: matches 2530. .2693 of consensus"
                                                                                                                                                                                                          678. .866
/note="MIR repeat: matches 35. .228 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1665. 5017
Mote="THE1B repeat: matches 1. 364 of consensus"
                                                                                                                                                                                                                                                                                                                                           complement(join(1450. .1559,1658. .>1808))
                                                                                                                                                                                           /note="match: STS: Em:HS499G10S"
678. .866
                                                                                                                        /note="match: GSS: Em:AQ389996"
101. .511
                                                                                                                                                       /note="match: GSS: Em:A0805436"
106. ,603
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/db_xref="taxon:9606"
/chromosome="20"
/clone="RP11-65K20"
                                                                                     /clone_lib="RPCI-11.1"
82. 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1485. .1490)
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Limb7" repeat: matches 6025. .6169 of consensus" 20428. .20602
/note="AluSx repeat: matches 1. .175 of consensus" a 4390 c 4131 g 5141 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFU43876 51 bp mRNA PRI 11-NOV-1998
Homo sapiens patient CS-1 clone AV3 T cell receptor alpha chain
AFO43876
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                                                                                                                                                                                                                                       17493. .17590
/note="MER20 repeat: matches 123. .212 of consensus"
complement(17719. .17955)
/note="match: GSS: Em:AQ019780"
18041. .1834
/note="Alux repeat: matches 1. .305 of consensus"
complement(19526. .19895)
/note="match: GSS: Em:AQ012075"
14630. .14756
/note="L2 repeat: matches 2620. .2750 of consensus"
14827. .15221
/note="match: STS: Em:HS574D2S"
14864. .15063
                                                                                                                                                      LTR33 repeat: matches 16. .201 of consensus" .16926
                                                                                                             /note="MER20 repeat: matches 16. 217 of consensus"
                                                                                                                                                                                                    note="MLT1B repeat: matches 2. .363 of consensus" 17493. .17590
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Strieblich, C.C., Falta, M.T., Wang, Y., Bill, J. and Kotzin, B.L.
Selective accumulation of related CD4+ T cell clones in the
synovial fluid of patients with rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Striebich, C.C., Falta, M.T., Wang, Y., Bill, J. and Kotzin, B.L. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 13
Gaps: 0
Percent Identity: 69.231
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/tissue_type="synovial fluid"
/clone="AV3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AL359534 from: 1 to: 20603
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                                                                                                                                          16381. .16558
/note="LTR33 re
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Align seg 1/1 to: S69140 from: 1
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                                      /note="Contains the 3' end of the TCRAV, the n, and the 5' end of the TCRAJ."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="from rheumatoid arthritis patient CS-1 [TCRAV1S3]
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strietich, C.C., Falta, M.T., Wang, Y., Bill, J. and Kotzin, B.L. Direct Submissions.

Bushitted (21-JAM-1998) Pediatrics, National Jewish Medical and Research Center, 1400 Jackson St., Denver, CO 80206, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AFU43877 51 bp mRNA PRI 11-NOV-1998
Homo sapiens patient CS-1 clone AV4 T cell receptor alpha chain
CDR3 (TCRA) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     striebich,C.C., Falta,M.T., Wang,Y., Bill,J. and Kotzin,B.L. selective accumulation of related CD4+ T cell clones in the synovial fluid of patients with rheumatoid arthritis J. Immunol. 161 (8), 4428-4436 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="T_cell receptor alpha chain CDR3"
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/db_xref="G1:3859384"
/translation="YFCAVRPSGSARQLTFG"
                                                                                     /product="T_cell receptor alpha chain CDR3"
/protein_id="AAC72676.1"
/db_xref="GI:3859382"
                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity: 73.333
                                                                                                                                             /translation="YFCAVRPSGSARQLTFG"
13 c 14 g 16 t
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/db_xref="taxon:9606"
/tissuc_type="synovial fluid"
/clone="AV4"
                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AF043876 from: 1 to: 51
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<1. .>51
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                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [TCRAJ22]"
/gene="TCRA"
                                /gene="TCRA"
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                                                                                                                                                                                                                                                      51.50
3.962
86.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_pr3:AF043877
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LOCUS AF043877
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08-881509-9 x AF043876
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Maggi.E. and Romagnani.S.
Molecular basis of cross-reactivity among allergen-specific human T cells: T-cell receptor V alpha gene usage and epitope structure Immunology 81 (1), 15-20 (1994)
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/note="This sequence comes from Fig. 3b; Protein sequence
is in conflict with the conceptual translation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCOS S69140 98 bp mRNA LOCOS DEFINITION TCR V alpha=T-cell receptor alpha-chain (allergen-specific) (human, grass-sensitive individual VI 19, peripheral blood, mRNA Partial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 98) Mohapatra, S.S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 144562] from the original journal article. This sequence comes from Fig. 3a.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-1994
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27 c 20 g 28 t
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/protein_id="AAB30244.1"
/db_xref="G1:545974"
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78.571 Percent Identity: 71.429
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                                                                             Percent Identity: 73.333
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/db_xref="taxon:9606"
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08-881509-9 x AF043877
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S69139.1 GI:545971
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85.714
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                                                              Homo sapiens
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LOCUS HSU40776
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Griesinger, F., Jansen, B. and Kersey, J.H.
Differentiation in mature T lymphoid leukemia cells is unstable and reversible to myeloid cells, without the involvement of a common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="METLLEVLSGTLLMQLTWVRSQQPVQSPQAVILREGEDAVINCS
SSKALYSVHWYROKHGEAPVFLMILLKGGEQKGHEKISASFNEKKQGSSLYLTASQLS
YSGTYFCGTASGSARQLTFGSGTQLTVLPDIQNPDPAVYQL"
                                                                                                                   LOCUS S63879 716 bp DNA PRI 04-MAY-2000 DEFINITION GENERAL TCell receptor variable alpha chain [human, MT-ALL,
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DEFINITION TCR V alpha-r-cell receptor alpha-chain (allergen-specific) (human, grass-sensitive individual VI 53, peripheral blood, mRNA Partial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation presented here differs from translation in
                                                                                                                                                                                                                                                                                                                                                                                                              GenBank staff at the National Library of Medicine created this entry [NCBI glbbsq 63879] from the original journal article. This sequence comes from Figure 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="This sequence comes from Figure 4; conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="T_cell receptor variable alpha chain"
/protein_id="AAB20291.1"
/db_xref="G1:238693"
1 TyrCysLeuAlaProSerGlySerAlaArgGlnLeuThrPhe 14
                       16 TICIGLEGECETACCIGGTICTGCAAGGAACTGACCITT 57
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85.714 Percent Identity: 71.429
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join(58. .109,340. .>716)
/gene="TCR V alpha"
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/db_xref="taxon:9606"
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                                                                                                                                                                                        S63879.1 GI:238692
                                                                                                    seq_documentation_block:
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                                                                   seq_name: gb_pr8:S63879
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08-881509-9 x S63879
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S69139
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Molecular basis of cross-reactivity among allergen-specific human T cells: T-cell receptor V alpha gene usage and epitope structure Immunology 81 (1), 15-20 (1994)
                                                                                                              1 (bases 1 to 98)
Mohapatra,S.s., Mohapatra,S., Yang,M., Ansari,A.A., Parronchi,P.,
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Waitkus, K., Boyle, L.A., Hishii, M. and Andrews, D. M.
T-call receptor usage by anti-melanoma specific cytotoxic tumor-infiltrating lymphocytes. Detection of dominant tumor-specific T-call clones by single strand conformational Unpublished (1955)
2 (bases 1 to 214)
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 214)
                                                                                                                                                                                                                                                                  94178804
GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 144561] from the original journal article.
This sequence comes from Fig. 3a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /exception="Protein Inger than coding region shown"
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/protein_id="AAB30243.1"
/db_xref="G1:545972"
/translation="DSATYFCAAPTGTASKLTFGTGTRLQVTLDIQN"
human peripheral blood grass-sensitive individual VI 53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="TCR V alpha"
/note="This sequence comes from Fig. 3b"
/codon_start=1
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/db_xref="taxon:9606"
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08-881509-9.rge

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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                             /product="T-cell receptor alpha chain"
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/db_xref="GT:1103937"
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SGSARQLTFGSGTQLTYLPDIQNPDPA"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Kurnick,J.T., Ihara,A., Pervaiz,S., Pandolfi,F., Van,Den Elsen P., Waitkus,R., Boyle,L.A., Hishii,M. and Andrews,D.M.
Direct Submission
Submitted (16-NOV1995) James T. Kurnick, Pathology Research
Laboratory, Massachusetts General Hospital, 149 East 13 St.,
Charlestown, MA 02129, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (09-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, Submitted (09-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk requests: clonerequest@sanger.ac.uk on Aug 11, 2000 this sequence version replaced gi:9211825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-AUG-2000
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Homo sapiens chromosome 1 clone RP5-88207 map p33-34.2, ***
SEQUENCING IN PROGRESS ***, 19 unordered viece.
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                                                                                                                                                                                                                 /cl_ne="MU 57"
/cell_type="cytotoxic T-cell lymphocyte"
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4.455 Gaps: 0
84.615 Percent Identity: 76.923
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                                                                                                                                                                                                                                                                                                                                                  /note="V alpha 2.1 J alpha 22"/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: SC
Web site: http://www.sanger.ac.uk
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                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                         Location/Qualifiers
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LOCUS AL136380 1
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08-881509-9 x HSU40776
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Consensus quality: 157434 bases at least Q30 consensus quality: 159115 bases at least Q20 consensus quality: 159115 bases at least Q20 lnsert size: 160556; sum-of-contigs Insert size: 164066; agarose-fp Quality coverage: 4.59x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is
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134647: contig of 25400 bp in length
14747: gap of 100 bp
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139480 155287; contig of 15808 bp in length
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96129 109147: contig of 13019 bp in length
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158545 162356: contig of 3812 bp in length.
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155288 158444: contig of 3057 bp in length
155388 158444: contig of 100 bp
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/note="assembly_fragment:00284
fragment_chain:1"
4190. .906
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/note="assembly_fragment:01422
fragment_chain:1"
fragment_chain:1"
26851. .37556
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fragment_chain:1"
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fragment_chain:1"
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69432: conti
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Alonce assembly fragment:00789
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41908...52345
fragment_chain:2"
52446...
58081
fragment_chain:3"
58182...
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fragment_chain:3"
58182...
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/note="assembly_fragment:00476
fragment_chain:2"
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Patent: EP 0816496-A 07-JAN-1998;
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Sequence 1 from Patent EP0816496.
A93127
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Schendel, D.J.
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Ratio: 4.083
Percent Similarity: 85.714
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ATMNYITAWOQPPSQGPRELIGGYKTKVTNEVASLEIPADRKSSTLSLPRVSLSDTAV
SQCKDSDAROLIFGSGTOLIVLPDIONPDPAVYOLROSKSBOKSVCLFTDEDSOTAV
SQCKDSDVYITDKTVLDMRSMDFKSNSAVAMSNKSDFACANAFNNSIIPEDTFFPSPE
SSCHOKLVEKSFETDTINLNFQNLSVIGFRILLLKVAGFNLLMTLRLMSS"

365 c 294 g 351 t
                                                                                                                                                                                                                                                                     /translation="MRQVARVIVFLTLSTLSLAKTTQPISMDSYEGQEVNITCSHNNI
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (21-MAR-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 37141)
DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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On Mar 21, 2000 this sequence version replaced 91:7021680.
Draft Sequence Produced by DOE Joint Genome Institute
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Gaps: 1
Percent Identity: 78.571
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Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
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                                                                                                                                                                          /note="unnamed protein product"
                                                                                                                                                                                                                         /protein_id="CAB69529.1"
                                                                      /organism="unidentified"
/db_xref="taxon:32644"
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BOEHRINGER MANNHEIM GMBH (DE)
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                            Location/Qualifiers
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DOE Joint Genome Institute.
Direct Submission
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                                                 1. .1341
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Percent Similarity: 92.857
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Unpublished
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LOCUS AC020943
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08-881509-9 x A93127
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This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 human chromosome 1, constructed by the Sanger Centre Chromosome 1 http://www.sanger.ac.uk/HGP/Chr1 { constructed at the Roswell Park 654H19 is from the library RPCI-4 constructed at the Roswell Park Cancer Institute by the group of pieter de Jong. For further cancer institute by the group of pieter de Jong. For further location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: AC020943 from: 1 to: 37141
                                                                                                                                                                                                           Length: 13
Gaps: 0
Percent Identity: 61.538
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/db_xref="taxon:9606"
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/chromosome="19"
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Location/Qualifiers
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AL049745.9 GI:5596759
HTG; CpG Island.
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Ratio: 4.000
Percent Similarity: 92.308
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3716. .9982
/note="LlMB3 repeat: matches 5897. .6182 of consensus"
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                                                                                                            116. .189
/note="AluSp/q repeat: matches 243. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5012. .5241
/note="L1M4 repeat: matches 4958. .5188 of consensus"
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/note="AluSq/x repeat: matches 1. .145 of consensus"
5760. 5928
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/note="AluJb repeat: matches 8. .296 of consensus"
17611. .17726
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hote="AluYa8 repeat: matches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AluSg repeat: matches 1. .297 of consensus" .12666
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                                                                                                                                                                                                                                                  'note="MLT1J repeat: matches 478. .501 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /_octe="Alusy repeat: matches 1. .300 of consensus" 11844. .12140 /note="Alusy repeat: matches 1. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anote="Allos repeat: matches 1. .295 of consensus" (6825. .17112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Alusc repeat: matches 1. .297 of consensus" 10757. .11071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71337 .11432
7note="AluSp repeat: matches 1. .295 of consensus"
11540. .11839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Fixa_A repeat: matches 2. .131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5242. .5497
/note="AluSx repeat: matches 1. .286 of consensus"
5542. .5597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="Alusx repeat: matches 1. .296 of consensus"
1576. .8860
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                                                                                                                                                                                                  1219. .1366
/note="L2 repeat: matches 2589. .2748 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Alu repeat: matches 247. .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="Alusg repeat: matches 1. .291 of consensus"
1257. .7440
                                                                                                                                                                                                                                                                                                                                                          /note="Alusx repeat: matches 1. .297 of consensus"
1698. .2155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4422. .4720
/note="AluSx repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MIR repeat: matches 53. .260 of consensus"
929. 8181
                                                                                                                                               534. .845
/hote="AluSc repeat: matches 1. .307 of consensus"
                                                                                                                                                                                                                                                                                                            /note="MITLIJ repeat: matches 1. .478 of consensus" 2203. .2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14572. 14729
//note="FAM repeat: matches 1. .159 of consensus"
16746. 16817
                                                                         /note="Alu repeat: matches 2. .62 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
/map="p31.1-33"
/clone_lib="RPCI-4"
/clone="RP4-654H19"
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/note="CpG island"
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/note="FLAM_C repeat: matches 2. 117 of consensus"
17748. 18038
/note="AluJo repeat: matches 1. 312 of consensus"
18973. >19967. >
18973. Separate in the sepa
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7004e="L1PB1 repeat: matches -239, .2030 of consensus"
30203. 31244
7004e="L1PB1 repeat: matches -1537. -412 of consensus"
71259. 31388
7004e="FLAM_C repeat: matches 1. 130 of consensus"
71548. 31527
7004e="FLAM_C repeat: matches 1. .102 of consensus"
7004e="FLAM_C repeat: matches 1. .102 of consensus"
7004e="Match: GSS: Em:B68328"
7004e="match: GSS: Em:A0355375"
7004e="match: GSS: Em:A0355375"
7101e="match: GSS: Em:A0355375"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 166. .256 of consensus"
20547. .20859
/note="Alusx repeat: matches 1. .306 of consensus"
21006. .13139
/note="Alusy repeat: matches 1. .306 of consensus"
/note="LiPA4 repeat: matches 6000. .6139 of consensus"
/note="MER30 repeat: matches 117. .175 of consensus"
21726. .22039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mote="Alusx repeat: matches 1. 297 of consensus" 23857. 23905 /mote="LiMe2 repeat: matches 6120. .6168 of consensus" 24372. .27627 /mote="LiPe1 repeat: matches 2030. .6155 of consensus" 27628 .27939
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23566. .23856
                                                                                                                                                                                                                                                                     //note="match: GSS: Em:AQ517971"
3434. .33650
/note="MALS" repeat: matches 47. .262 of consensus"
34737. .35046
/note="AllSx repeat: matches 1. .310 of consensus"
59526. .36218
/note="AllSx repeat: matches 1. .293 of consensus"
36537. .36837 repeat: matches 32. .308 of consensus"
/note="AllUO repeat: matches 32. .308 of consensus"
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22040. .22159
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22376. .22636
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/note="L2 repeat: matches 2455. .2659 of consensus"
38141. .38437
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27940. .30182
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/note="match: GSS: Em:AQ237932" 23210. .23565
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/note="Alur repeat: matches 1. 297 of consensus"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 135935)
                                                                                                               /note="AllSgl repeat: matches 1. .303 of consensus" 41816 .41867 /note="LIMA9 repeat: matches 6235 .6285 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (22-A0G-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 25, 2000 this sequence version replaced gi:9801504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AL391003 135935 bp DNA HTG 23-AUG-2000
DEFINITION Homo sapiens chromosome 1 clone RP11-205P11, *** SEQUENCING IN
PROGRESS ***, 29 unordered pieces
                  /note="AluJo repeat: matches 13. 299 of consensus" 39983. .40251
/note="AluSx repeat: matches 15. 297 of consensus" 41387. .41678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid: LO8752; 100% of reads Chemistry: bye-terminator Big Dye; 40% of reads Chemistry: Dye-terminator ET-amersham; 59% of reads quality: 119874 bases at least Q40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Consensus quality: 125595 bases at least Q30 Consensus quality: 129421 bases at least Q20 Insert size: 133135; sum.of-contigs linsert size: 1614949; 9.5% error; agarose-fp Quality coverage: 3.50x in Q20 bases; sum-of-contigs Quality coverage: 2.89x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: HSJ654H19 from: 1 to: 117493
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                                                                                                                                                                                                                                                   Percent Similarity: 91.667 Percent Identity: 75.000
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Web site: http://www.sanger.ac.uk
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  39317. .39614
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Quality:
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KEYWORDS
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100 bp

/note="Alujb repeat: matches 1. .280 of consensus"

Page 10

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99/50

98/62 98161: gap of

98162 102868: contig of 4707 bp in length

102869 102968: gap of

102869 102968: gap of

10545 105644: gap of

105545 105644: gap of

105645 108601: contig of 2576 bp in length

108601 108700: gap of

108601 108700: gap of

119556 119555: contig of 100 bp

119556 119555: gap of

119556 119555: gap of

119656 125691: contig of 6036 bp in length

125792 125791: gap of

125792 125791: gap of

100 bp
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79187 83825: contig of 4639 bp in length
83826 83925: gap of 100 bp
83926 88162: contig of 4237 bp in length
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75981: contig of 3912 bp in length
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76082 79086: contig of 3005 bp in length
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30942 38597: contig of 7656 bp in length
38598 38697: gap of 100 bp
38698 41812: contig of 3115 bp in length
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                     10237 10336: gap of 100 bp 10337 12524: contig of 2188 bp in length 12525 12624: gap of 100 bp 12525 12624: gap of 9164 bp in length 12625
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21889 24154: contig of 2266 bp in length
24155 24254: gap of 100 bp
24255 27622: contig of 3368 bp in length
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27723 30841: contig of 3119 bp in length
10236; contig of 6663 bp in length
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24255. .27622
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'note="assembly_fragment:00153"
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/clone_lib="RPCI-11.1"
1. .3473
/note="assembly_fragment:00103"
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/note="assembly_fragment:00146"
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/note="assembly_fragment:00158"
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/db_xref="taxon:9606"
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129999 135935: conti
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98061: cont.
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                                                                                                                                                                                                                                                                                                                                                                                          51136 51235: gap of
51236 54324: cont
                                                                                                                                                                                                                                                                                                                                            41813 41912: gap of
41913 51135: cont
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2817 others
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Gaps: 0
Percent Identity: 75.000
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/note="assembly_fragment:01129"
95750. .98061
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98162. .102868
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/note="assembly_fragment:00858"

/note="assembly_fragment:00903"

/note="assembly_fragment:00942"

/note="assembly_fragment:00942"

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108701. 119555
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129999. 135935
/note="assembly_fragment:01439"
1 28565 c 28908 g 37331 t 28
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                                                                                 /note="assembly_fragment:00503"
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Percent Similarity: 91.667
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Gaps: 0
Percent Identity: 100.000
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/isolate="patients 22 and 26"
/db_xref="taxon:9606"
                                              1.0e+04
1.0e+04
1.0e+04
1.0e+04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1 from Patent EP0816496.
A93127
                                              87.68
87.58
87.36
87.30
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Jantzer, P.
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Percent Similarity: 100.000
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08-881509-10 x HSTCRJUNC
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LOCUS A93127
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                                    gb_htg10:AC024233
gb_htg9:AC022528
gb_htg5:AC015711
gb_pr3:AC012531
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                                                                                                                                                                                                                                                                                                                      DEFINITION
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                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
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AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 re Len | Documentation | 1318 | X88410 H.sapiens mRNA for rear | 9 | 134 | X89410 H.sapiens mRNA for rear | 995 | AL144658 Anopheles gambiae STS | 37751 | 283864 Mycobacterium tubercul | 174788 | AP000756 Homo sapiens chrome | 185286 | AC016721 Homo sapiens chrome | 186787 | AC075557 Homo sapiens chrome | 186787 | AC07557 Homo sapiens chrome | 1735 | 235133 B.subillis 168 pks general | 17447 | AC006444 Homo sapiens PAC cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 | ACC23303 Homo sapiens chromo-

741 | ACC02342 Human BAC clone CTF

780 | 299113 Bacillus subtilis com-

781 | ACC0242 Human BAC clone CTF

780 | AFCV9139 Streptomyces venezuel

781 | ACC05119 Drosophila melanogas

782 | ACC02475 Human BAC clone GSI

783 | ACC02478 Human BAC clone GSI

784 | ACC06303 Homo sapiens chromo-

785 | ACC06303 Homo sapiens chromo-

786 | APCO2480 Oryza sativa genomi-

787 | ACC06909 Homo sapiens chromo-

788 | ACC06303 Homo sapiens chromo-

789 | ACC06303 Homo sapiens chromo-

789 | ACC06303 Homo sapiens chromo-

789 | ACC06903 Homo sapiens chromo-

789 | ACC06903 Homo sapiens chromo-

780 | ACC06903 Homo-

780 | ACC06903 Homo-

780 | ACC06000 Homo-

780 | ACC0600 Homo-

780 | ACC060 Ho
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                                                                                                                                                                                                                                          ! AC025799 Homo sapiens chromo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC027112 Homo sapiens chromc
AC083898 Homo sapiens chromd
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AC015947 Homo sapiens clone
AC024329 Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL122029 Drosophila melanoga
AL121947 Human DNA sequence
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                                                                                                                             About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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34423
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98874
OM of: 08-881509-10 to: GenEmbl:* out_format : pfs
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3.3e+03
3.3e+03
4.9e+03
4.9e+03
5.6e+03
6.4e+03
7.0e+03
7.4e+03
1.9e+03
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2.0e+03
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1.4e+03
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Database sequences: 1118133
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Search time (sec): 3669.820000
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Query length: 13
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9b_pr6:HS696P19
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9b_htg19:AL157697
9b_htg24:DMBR12B22
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9b_htg216:AC009099
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9b_htg18:AC079128
9b_ltg18:AC079128
9b_itg18:ARF001678
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gb_htg9:AC023303
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gb_htg24:DMBR42L18
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gb_htg16:AC069303
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9b_sts1:CNS01HNL
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gb_ba2:BSUB0010
gb_ba1:AF079139
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gb_htg7:AC019767
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| ACO24233 Homo saptens chr
| ACO22528 Homo saptens chr
| ACO15711 Homo saptens chr
| ACO12531 Homo saptens, cl
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1318)
Jantzer, P. U. and Schendel, D. J.
Tumor-infilltrating lymphocytes recognizing spontaneously arising
renal call carcinomas express T cell receptors characteristic of a
secondary immune response
                                                                                                                                                                                           X98410.1 GI:1770560
J gene; junction; T cell receptor; TCR junctional sequence; V gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ourset Submission
Submitted (11-JUN-1996) P. Jantzer, Institute for Immunology,
Goethestr. 31, D- 80336 Munich, FRG
Location/Qualifiers
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                                                                                                                                      HSTCRJUNC 1318 bp mRNA PRI 08-JA
H.sapiens mRNA for rearranged TCR junctional sequences.
X98410
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                                                                                                                                                                                                                                                                                                                                                                                                ATNDYITWYQOFDSGGPRFIIQGYKTKVTNBVASLFIPADRKSSTLSLPRVSLSDTAV
YYCLVGGSARQLTFGSGTQLTVLPDIONPDPAVYQLRDSKSSDKSVCLFTDFDSQTNV
SQSKDSDVYITDKTVLDMRSMDFKSNSAVAMSNKSDFACANAFNNSIIPEDTFFPSPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles gambiae STS SP6 end of clone 09007 of Notrebamel library from strain PEST of Anopheles gambiae (African malaria mosquito), sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                     /db_xref="G1:6741517"
/translation="MRQVARVIVFLTLSTLSLAKTTQPISMDSYEGGEVNITCSHNNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France Roux, Paris 75015, France This clone is from an A. gambiae BAC library provided by F.H. This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae; Anopheles.
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Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
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92.308 Percent Identity: 92.308
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                                                                                                                                                                                                                                                                                                        /note="unnamed protein product"
                                                                                                         Schendel, D.J.
T-cells specific for kidney carcinoma
Patent: EP 0816496-A 07.7AN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
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                                                                                                                                                                                                                                                                                                                                              /protein_id="CAB69529.1"
                                                                                                                                                                                                                     /organism="unidentified"
/db_xref="taxon:32644"
                                                                                                                                                                                      Location/Qualifiers
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365 c
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08-881509-10 x A93127
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tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk on Jun 27, 1998 this sequence version replaced 91:1781088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.
283864 AL123456
283864.1 GI:3261687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis
Bacteria, Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erratum:[[published erratum appears in Nature 1998 Nov 12;396(6707):190]]
                                                                                                                                                                                         3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: CNSO1HNL from: 1 to: 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCT
                                                                                                                                                                                                                                                                                                      Length: 13
Gaps: 0
Percent Identity: 61.538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TyrCysLeuValGlyArgSerAlaArgGlnLeuThrPhe 13
                                                 /organism="Anopheles gambiae"
                                                                                                                                                                                         269 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete genome sequence
Nature 393 (6685), 537-544 (1998)
98295987
                                                                                                                                             /clone_lib="NotreDame1"
                                                                                         /db_xref="taxon:7165"
/clone="09C07"
                                                                                                                                               /clone_lub ...
/note="end: SP6"
/note="end: 216 g
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 37751)
                                                                          /strain="PEST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37751 bp
                                                                                                                                                                                                                                                                                                                                    Ratio: 3.769
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                08-881509-10 \times CNSO1HNL/rev
                                                                                                                                                                                                                                                                                                                49.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_ba2:MTCY1A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkhill, J
                                                                                                                                                                                                 Ø
                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MTCY1A6
                                                                                                                                                                                                 285
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                                                                                                                                                                                                                                                                                                 alignment_scores:
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CDS

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Complement(48. 677)
/gene="Rv3830c"

complement(48. 677)
/gene="Rv3830c, (MTCY01A6.39), len: 209. Probable
transcriptional regulator, similar to TCMR_STRGA P39885
tetracenomycin c transcriptional repressor (226 aa), fasta
scores, opt: 255, E(): 1.9e-11, (33.7% identity in 20.2aa
overlap). Contains possiblehelix-turn-helix motif from aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MVRPPQTARSERTREALRQAALVRFLAQGVEATSAEQIAEDDAGV
SLRTFYRHFRSKHDLLFADYDAGLHWFRAALDARPADESIIDSVQAALFSFPYDYDAV
KIASLRRGELEPSRIVRHWREVEADFADAIQAQLRRRNCDIAGAPDARLHIAVTARC
VAAAVFGABWMLGSDRSLGELARVCHVALESLRVGISDTWTTLTVSS"
749. .1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MVSLLVHAALGVVVIGWIVSSNPKVFTRPAGGSWFSLPECVYYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGIASIALGWYFNIRFVQQYAHGAANPLWGPGSWAEYVRLMFTNPAASSAGQDYTIAN
VILLPLFSTTDGYRRGLRRPWLYFVSSLFTSFAFAFAFYFATIERQHRHERSRATVGA
                    CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation-"MAMNLLHRRHCSSAGWEKAVANOLLPWALQHVELGPRTLEIGPG
YGATLQALLGLTASLTAVEVDNSMVERLNRRYGQRARIIRGDGTQTGLEDDHFTSVVC
FTMLHHVASAQLQDQLFAEAYRVLQPGGVFAGSDGVPSLPFRLIHIADTYTPIAPADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Rv3833, (MTCY01A6.36c), len: 263. Possible
transcriptional regulator, similar to e.g. YFIE_BACSU
an increase in the observed/expected third position {\tt G} + {\tt C}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Rv3832c, (MTCY01A6.37), len: 191. Unknown."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Rv3831, (MTCY01A6.38c), len: 160. Unknown"
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/protein_id="CAB06211.1"
/db_xref="G1:1781127"
                                                                                                                                                                                                                                              /organism="Mycobacterium tuberculosis"
                                                                                                                                                                                                                                                                                                                                                     /organism="Mycobacterium tuberculosis"
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/product="hypothetical protein Rv3832c"
/protein_id="CAB06209.1"
/db_xref="G1:1781125"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein Rv3831"
/protein_id="CAB06210.1"
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/db_xref="SPTREMBL:P96247"
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/gene="Rv3832c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1228. .1803)
                                                                                                                                                                                                                                                                                                       /db_xref="taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"taxon:1773"
                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
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                                                                                                                                                                                                                                                                           train-"H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                     /strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Rv3831"
749. .1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Rv3832c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="Rv3831"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="YlA6"
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/note="Rv3833,
                                                                                                                                                                                                                                                                                                                                    .37447
                                                                                                                                                              initiation codon.
                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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                                                                                                                                                                                       FEATURES
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/note="Rv3834c, (MTCY01A6.35), len: 419. Seryl-trna
Synthetase, similar eg to SYS_BACSU P37464 (425 aa), fasta
Scores, opt: 1015, E(): 0, (39.3% identity in 425 aa
overlap): contains PS00179 Aminoacyl-transfer RNA
                                                                                                                                                                                                                                                                                                                              HAGTWITPVNRAIWIPAGCWHQHKFHGHTQFHGVALDPQRYRGGPATPTVLAVNPLMR
P54722 hypothetical transcriptional regulator (314 aa), fasta scores, opt: 171, E(): 8.5e-05, (30.2% identity in 126 aa overlap). Contains probable helix-turn-helix motif from aa 165-186."
                                                                                                                                                                                                                                                                  /db_xref="SPTREMBL:P96245"
/translation="MSENSHHRLATTSLTLPPGARIERHRHPSHQIVYPSAGAVSVTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLTGRGALLQLGLLQLALKLAVDNGFVPTIPPVLYRPEYMVGTGFLGHHABEVYRVEG
GGZIVUGTSEYVPLAGYHSGEILDLSRGPLRYAGWSSCFRREAGSHGKDTRGIIRVHQF
DKVEGFVYCTPADAEHEHRLLGWQRQMLARIEVPYRYIDVAAGDLGSSAARKFDCEA
WIPTQGAYRELTSTROTTFQARRLATFYRDASGKPQIAATLNGTLATTRWLVAILEN
HQRPDGSVRVPDALVPFVGVEVLEPVA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADSLRAEQKAASKSVGGASPEERPPLLRRAKĒLAEQVKAAEADEVEAEAAFTAAHLAI
SNVIVDGVPAGGEDDYAVLDVVGEPSYLENPKDHLELGESLGLIDMQRGAKVSGSRFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / LTAIGELIOR-WILDAPEODPUDECDPASPPHGEAEOPLEGPRWFRALRASATRRA LLLTALGGLLIAGLVTAIPAVGRAPERLAGYIASVDPHGEAEORYDSTGAKINASFNRYASGDCLM PROFTPESTAIVSCADEHRFEYAESIDMRTPECMEYCONAAPPSPAIROOTSEEGCEA AVRRYLGTKEDPANSETISMUNGCBRRACAGERRALGGLOSPGPNNOOLAFKGYAD IDOSKWWPAGTCLGIDATTNOPIDVPVDCAAPHAMEVSGTVMILAERFPDALFSEPEGO GEIKDACTRWIDAYLAFLKETTITLIYVTILYPTLTLESWSAGSRYVACSIGATLGNGGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"MIDLKLLRENPDAVRRSQLSRGEDPALVDALLTADAARRAVIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLVNSAKGALLINGOPPVPPDIPEBRLNLPPIPLQLPTPRRAPPAQQLBSTPPGTQH
LPAQQPVVTPTRPPESHAPASAAPAETQPPPPDAGAPPATGSPEATPPGBAEPAPG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Rv3835, (MTCY01A6.34c), len: 449. Unknown."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     //ote="PS00179 Aminoacyl-transfer RNA synthetases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Rv3836, (MTCY01A6.33c), len: 137. Unknown; containsPS00142 Neutral zinc metallopeptidases, zinc-binding regionsignature" /codo_binding regionsignature" //ransl_table=11 //product="hypothetical protein Rv3836" /product="CAR06205.1" //product="CAR06205.1" //product="C1:1781121"
                                                                                                                                                                                    /product="hypothetical protein Rv3833"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="hypothetical protein Rv3835"
/protein_id="CAB06206.1"
/db_xref="G1:1781122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthetases class-II signature 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAB06207.1"
/db_xref="G1:1781123"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2647. .3906)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2647. .3906)
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                                                                                                                                                                                                                                         /db_xref="GI:1781124"
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                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/transl_table=11
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/transl_table=11
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/gene="Rv3836"
5393. .5806
/gene="Rv3836"
                                                                                                                         /codon_start=1
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/gene="Rv3835"
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CDS

gene

CDS

/db_xref="SPTREMBL:P96242"

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NOTE: This is a 'working draft' sequence. It currently consists of
/translation="mtvrmdpQredELVSDALDLIPPELADAMDNVVVLVANRHPQHE
NLLGQYEGYALTERCSDYAGSLPDAITIYREALLDACDSEDEVVDQVAITVIHEVAHH
FGIDDERLDQLGWRDEPAPGRGNPDLSAPDAMNGP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-NOV-1999) to the DDBJ/EWBL/GenBank databases. Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC): 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattoridgsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924) on Sep 15, 2000 this sequence version replaced gi:8118915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG 14-SEP-2000 HOMO Sapiens chromosome 11 clone RP11-720D4 map 11q14, WORKING DRAFT SEQUENCE, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 173888; sum-of-contigs
Quality coverage: 12.08x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 consensus quality: 171368 bases at least 040 consensus quality: 172579 bases at least 030 consensus quality: 17326 bases at least 020
                                                                                                          /note="PS00142 Neutral zinc metallopeptidases, zinc-binding region signature" complement(6001. .6699)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: RIKEN Genomic Sciences Center(GSC)
                                                                                                                                                                                                                                                                              Percent Identity: 81.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: HumDraft11
                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      19929 IGCATTGTGGCCGTTCGCGCGCGCGCTAACC 19961
                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-720D4.
                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: MTCY1A6 from: 1 to: 37751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone name: RP11-720D4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Center
                                                                                                                                                                            /gene="Rv3837c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AP000756.3 GI:10130041
                                                                           5672. .5701
/gene="Rv3836"
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                                                                                                                                                                                                                                                                Ratio: 4.700
Percent Similarity: 90.909
                                                                                                                                                                                                                                            47.00
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LOCUS AP000756 17
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Ratio:
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Homo sapiens chromosome 2 clone RP11-327J6, WORKING DRAFT SEQUENCE, 19 unordered pleces.
10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //note=massembly_fragment"
164588..170558..170587
/note=massembly_fragment clone_end:SP6 vector_side:left"
170659..172080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121965. .136845
/note="assembly_fragment clone_end:T7 vector_side:left"
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                                                                  are unknown. This record will be updated with the inisined as soon as it is available and the accession number will be
                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                 14881 bp in length
17017 bp in length
10425 bp in length
5971 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         900 others
                                                                                                                                                                                                                                      1422 bp in length
1382 bp in length
1126 bp in length.
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172181. .173562
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154063. .164487
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173663. .174788
/note="assembly_fragment"
a 32826 c 32654 g 54605
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94101. .121864
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                                                                                                                                                121864 contig of
136845 contig of
153962 contig of
164487 contig of
170558 contig of
                                                                                                                  contig of contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="11"
/clone="RP11-720D4"
/map="11q14"
1 62406
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08-881509-10 x AP000756/rev
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170659
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ORGANISM

KEYWORDS

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

TITLE

REFERENCE AUTHORS

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46 104451: contig of 11806 bp in length 152 104551: gap of unknown length 152 121910: contig of 17359 bp in length 11 122010: gap of unknown length 11 134398: contig of 12388 bp in length 19 134398: contig of 12387 bp in length 15877: contig of 23879 bp in length 178 158477: gap of unknown length 178 158477: gap of unknown length 178 15826: contig of 26809 bp in length 185286: contig of 26809 bp in length.
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122011. 134398
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134499. 158377
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158478. 185286
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54 a 32166 c 32604 g 58737 t 182
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31753. .38667
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.04552. .121910
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/note="assembly_name:Contig6"
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                                                                                                                                                                                                                                                                                                          'note="assembly_name:Contig4"
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11728. .18380
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/chromosome="2"
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                                                                                                                                                                                                                                                                        /clone="RP11-327J6"
                                                                                                                                                                                                                                                                                                                                                                                                                     vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                        6283. .11627
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08-881509-10 x AC016721/rev
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Percent Similarity:
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                                                                                                                                                                                            Direct Submission
Submitted (04-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia! Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 185286)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                 MO 63108, USA
On Mar 13, 2000 this sequence version replaced gi:7022633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: plasmid: 19% Chemistry: Dye-primer ET; 81% of reads Chemistry: Dye-terminator Big Dye; 19% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 173248 bases at least Q40 Consensus quality: 177028 bases at least Q30 Consensus quality: 177193 bases at least Q30 Insert size: 185Kb; agazose-fp Insert size: 185Kb; agazose-fp Ouality coverage: 4.00 in Q20 bases; agarose-fp Quality coverage: 4.00 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                        Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                  Center project name: H-M19327006
Sequencing vector: M13, 81%
                                                                                                                                                                                                                                                                                                                                                            Web site:http://genome.wustl.edu/gsc/index.shtml
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contig of 5345 bp in length
gap of unknown length
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contig of 2694 bp in length
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contig of 2236 bp in length
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of 5997 bp in length
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of 6915 bp in length
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                                                                                                                                                                                                                                                                                                              ------ Genome Center ------
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                                                                                                                The sequence of Homo sapiens clone Unpublished 2 (bases 1 to 185286)
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                              Homo sapiens
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DEFINITION

ACCESSION

KEYWORDS

VERSION SOURCE

ORGANISM

AUTHORS REFERENCE

JOURNAL REFERENCE AUTHORS

TITLE

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3075: contig of 3075 bp in length
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/db_xref="taxon:9606"
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34786: 786: 86
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68134: cont
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60061; cont
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43633: cont
                                                                                                                                                                       ): gap of
6653: con
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8407 32482: cor
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3176 4344: co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E (bases 1 to 186787)

B Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Badderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Colangelo, M., Collins, S., Collymore, A., Castler, A., Cabangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FilzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grart, G., Hagos, B., Heaford, A., Horton, L., Karadas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McBwan, P., McGurk, A., McKernan, K., McPara, S., McCarthy, M., McBwan, P., McGurk, A., McKernan, K., Menga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollvar, T. M., Ollver, J., Peterson, K., Pierre, M., Schauer, S., Schaue
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                        Homo sapiens chromosome 2 clone RP11-70708 map 2, WORKING DRAFT SEQUENCE, 30 unordered pieces.
                                                                                                     04-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality coverage: 4.2 in Q20 bases; agarose-fp Quality coverage: 4.4 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-terminator Big Bye: 100% of reads Assembly program: Phrap: version 0.960731 consensus quality: 1/2765 bases at least 030 consensus quality: 1/9967 bases at least 030 consensus quality: 182697 bases at least 020
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                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 186787)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Unpublished
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Insert size: 183887; sum-of-contigs
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                                                                                                                                                                                                                   AC073557.2 GI:10567944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 186787)
                                                                               seq_documentation_block:
LOCUS AC073557 186787 bp
                  seq_name: gb_htg17:AC073557
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                                                                                                                                                                                                                                                                                               human.
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TITLE JOURNAL

COMMENT

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8519 85518: gap of 100 bp 85519 92963 93062: contig of 7444 bp in length 92963 93062: gap of 100 bp 93063 100676: gap of 100 bp 100677 100776: gap of 100 bp 10077 110361: contig of 9385 bp in length 110362 110461: gap of 100 bp 110362 110461: gap of 100 bp 120398 120497: gap of 100 bp 120398 120497: gap of 100 bp 120398 120497: gap of 100 bp 120498 129640: contig of 9135 bp in length 120498 129640: contig of 9135 bp in length
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156311 169999; contig of 13689 bp in length
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170100 185820; contig of 15721 bp in length
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185921 186787: contig of 867 bp in length.
                                                                                                                                                                                                     of 100 bp contig of 24076 bp in length
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contig of 4705 bp in length
contig of 1169 bp in length of 100 bp contig of 1169 bp in length of 100 bp
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33676: contig of 1094 bp in length
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37514: contig of 2628 bp in length
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40126: contig of 2512 bp in length
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51189. 54290
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alignment_scores:

Quality: 47.00 Ratio: 3.917 Percent Similarity: 92.308 alignment_block: 08-881509-10 x AC073557 ..

Length: 13 Gaps: 0 Percent Identity: 53.846

Align seg 1/1 to: AC073557 from: 1 to: 186787

1 TyrCysLeuValGlyArgserAlaArgGlnLeuThrPhe 13 |||||||:::::|||::: |||:::|||||| |101773 TACTGTGTCTTAGGCAATAGAGCTAAACAGATAACATTT 101811

seq_name: gb_in3:TSAJ9167

23-MAR-2000	Trypanosomatidae; humans and primates (1998)	Gibson,W.C. human pathogenic ruzi	Biological Bristol, BS8 lUG,	·							22-AUG. ynthase. Bacilla	, Tognoni,A., Grandi,G., polypeptide highly
documentation_block: SE TSAJ9167 2130 bp DNA INV NITION Trypanosoma sp. 188 rRNA gene, isolate K&A. SSION AN009167 ION AN009167 ORDS 188 ribosomal RNA; 188 rRNA gene. CE Trypanosoma sp.	ienozoa; Kinetoplastida; 2130) yes,H. and Gibson,W. Cf trypenosomes infecting aldo Cruz 93 (5), 669-676	1 to 2130) 7.R., Noyes, H.A., Dover, G.A. and ent and divergent origins of the mmes, Trypanosoma brucei and T. cogy 118 (Pt 1), 107-116 (1999)	Stevens, J. R. Stevens, J. R. Submission Submitted (17-JUN-1998) Stevens J. R., School of Sciences, University of Bristol, Woodland Road,	Location/Qualifiers 1. 2130 /organism="Trypanosoma sp." /isolate="KgA" /strain="Leech" /db_xref="taxon:5696" <1. >>230	/gene="18S rRNA" /product="18S rlbosomal RNA subunit" 1 2130 /gene="18S rRNA"		scores: Quality: 45.00 Length: 10 Ratio: 4.500 Gaps: 0 imilarity: 100.000 Percent Identity: 80.000	TSAJ9167	Steuvaldlyargseralaargdin 10	gb_ba2:BSPOLKET	7735 bp DNA 168 pks gene for putati 1510952 19yetide synthase. otilis rmicutes; Bacillus/Clc	Scottl,C., Platti,M., Cuzzoni,A., Perani,P., Tog Galizzi,A. and Albertini,A.M. A Bacillus subtilis large ORF coding for a poly
seq_documer LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL MEDITME	REFERENCE AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOURCE IRNA	gene	BASE COUNT ORIGIN	ignment_ ercent S	alignment_block: 08-881509-10 x Align seq 1/1	1 6	seq_name: gb	seq_documentation_block LOCUS BSPOLKET DEFINITION B.Subtlifs ACCESSION 235133.1 G KEYWORDS PKS gene; pSOURCE Bacillus sull ORGANISM Bacillus. Bacillus. REFERENCE 1 (bases 1 Arminoscient Course Cours	

LHPSLMDSAFHATVGFIVSSVNAAGQAQTLSLPFALQEVDIFSPCPEKIWSYIRYSSD

TITLE JOURNAL AUTHORS

FEATURES

CDS

MEDLINE REFERENCE AUTHORS JOURNAL REFERENCE

JOURNAL

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KGMRAGVYIGGRSQHKPDPASLSKAKNDIVAGGQNYLAANISQFFDLKGPSILLDTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALEKSGKKTEEISYLEANGSGSAVTDLLELKAIOSIYRSESKAPLGLGSVKPNIGHPL
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                                                                                                                                                                                              Direct Submission
Submitted (11-JUL-1994) Grandi G., Eniricerche S.P.A., Genetic Submitted (11-JUL-1994) Grandi G., Eniricerche S.P.A., Genetic Engineering and Microbiology, Via F. Maritano, 26, S. Donato Milanese (MI), Italy, 20097
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative polyketide synthase ORF2"
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                                                                                                                                                                                 Grandi, G.
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RBS

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Submitted (10-JUL-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA (bases 1 to 127447)
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Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 24, 1999 this sequence version replaced gi:4139379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-JAN-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 127447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (24-MAR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                 WAYRNOOWHOOOLIPYRSSLSGDTIYRKGGYVVVIGGAGYIGEAWSEYMIRRYQAQIV
WIGRSQLNAALOSKIDRLSALGPEPFYIAADAADKHSLQOAYEQYKRHPHIHGIVHS
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SHYASGCTFADAFAHQLSQSNACPVVWNWGYWGNSEAAEDEHYVQLMNQIGLGLIEP
ARAMKALEALLSGPYGOTAFHHTTRPVAVEGVNQNEF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC006344 127447 bp DNA PRI 21-DEC-1999
Homo sapiens PAC clone RP4-726N20 from 7q32-q34, complete sequence.
AC006344
SKAENKVRKYDIDLODENGRYCVRMGASMRALDGEGHSKPOLLTDSOLTGHTVMIPV
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                                                                PVTQHEAVQPAHASIHGLAGTMAKEYPHWKIRLLDLEKGCTWPVNHMFALPADRLGHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cordes,M., Wohldman,P., Pape,K. and Hotic,M.
The sequence of Homo sapiens PAC clone RP4-726N20
                                                                                                                                                                                                                                                                                                                     7650 CACTGCTTTCTGGGCCAGTCAGCCAAACAGCTTTCATTC 7688
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Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. B (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TyrCysLeuValGlyArgSerAlaArgGlnLeuThrPhe 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: BSPOLKET from: 1 to: 7735
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Waterston, R.H.
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08-881509-10 x BSPOLKET
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Locus AC006344 11
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Center: Washington University Genome Sequencing Center
                          Center code: WúGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson wustl.edu
Contact: Summary Statistics
                                                                                                                                        Center project name: H_DJ0726N20
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted: restriction digest.

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information http://www.nhgrlin.h.gov/DIR/GTB/CHR7, send http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc MAPPING INFORMATION:

This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://Dacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from SOURCE INFORMATION: one male donor,

The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.

The clone sequenced to the left is RP4-529P3. Actual start of this clone is at base position 1 of RP4-726N20; actual end is at 127447 VECTOR: pCYPAC2 NEIGHBORING SEQUENCE INFORMATION:

The run of A's from 48936 to 48936 may contain one less A, no read

of RP4-726N20.

was able to make an exact call. Location/Qualifiers FEATURES

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   .127447
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repeat_region

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join(<3755. .4006,6362. .6490,7525. .7578,11428. .11568)

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/note="verified by mouse ESTS AA617614 (NID:g2504819) and

AA237696 (NID:g1861718); H_DJ0726N20.1"
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4836. 5222
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3957. 4006
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6362. 4900

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5739. .6032 /rpt_family="AT_rich"
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6359. .649A
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4198. .4496
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1497. .4637
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Center: Whitehead Institute/ MIT Center for Genome Research
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of 941 bp in length
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1745, 2685: contig of
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9483: contig of
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6018: contig of
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.----- Genome Center
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82856: cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L., Nusbeum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Daver, P., Fitzugh, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, C., Than, L., Carner, G., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Londers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McRenna, K., McPheerers, R., Meldrin, J., Meneus, L., Mihova, T., Mitanda, C., McPheerers, N., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Pisani, C., Pollara, Y., Raymon, C., Riley, R., Spencer, B., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, N., Vo, W., Wilson, B., Wu, X., Myman, D., Ye, W., Direct, C., Wang, C., Walley, M., Travers, M., Trayers, M., Tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Apr 3, 2000 this sequence version replaced gi:7239685.

• All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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LOCUS AC025799 152512 bp DNA AC025799 15. WORKING DREFINITION Homo sapiens chromosome 15 clone RP11-695JZ0 map 15, WORKING DRAFT SEQUENCE, 13 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152512)
                                                                                                                                                                          7523. .7578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: AC006344 from: 1 to: 127447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 66.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
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                                         /rpt_family="Alu"
7523. .7578
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08-881509-10 x AC006344/rev
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KEYWORDS
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                           Center project nume: 18221
Center project name: 18221
Center clone name: 692_2020
Center clone name: 692_202
Sequencing vector: M13 M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 14519 bases at least 040
Consensus quality: 146867 bases at least 020
Consensus quality: 150120 bases at least 020
Insert size: 150000; agarose-fp
Insert size: 151312; sum-of-contigs
Quality coverage: 4.4 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32233; gap of 100 bp 40916; contig of 8683 bp in length 41016; app of 100 bp 50385; contig of 9369 bp in length 50485; gap of 6725; contig of 15240 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102408 102507; gap of 100 bp 102508 152512; contig of 50005 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    p of 100 bp contig of 17031 bp in length
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82957 102407: contig of 19451 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16010: gap of ______ 100 bp ______ 22485; contig of 6475 bp in length 22585; gap of _______ 100 bp ______ 32133: contig of 9548 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 bp
f 3233 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 bp
of 3365 bp in length
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23415
                                                                                      JOURNAL
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Buthon,L. Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavkiy,L., Boukhaglater,B. Brown,A. Burkett,G. Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M., Doyle,M., Deyer,C., J. Ferreira,P., FitzHugh,W., Forrest,C., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Illev,I., Johnson,R., Jones,C., Kann,L., Klein,J., Landers,T., Largocque,K., Lehocckk,J., Levine,R., Lieu,C., Liu,G., Looke,K., Macdonald,P., Marquis,N., McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Minga,V., Raymond,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M., Riley,R., Rogov,P., Rothman,D., Santos,R., Schauer,S., Severy,P., Spencer,B., Stenge-Thomann,N., Satojanovic,N., Tirrell,A., Travers,M., Trigillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS AC023303 169181 bp DNA HTG 26-MAY-2000
DEFINITION Homo sapiens clone RP11-28L11, WORKING DRAFT SEQUENCE, 26 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 169181)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                          1201 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AC025799 from: 1 to: 152512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 81.818
                                                                                                                                                                                                                                                                                                                                                                                               vector_side:right"
a 26845 c 27061 g 48178 t
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                                                                                                                                       Length:
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    16011. .22485
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                                                                                                            /note="assembly_fragment"
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                                                                                             .40916
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08-881509-10 x AC025799/rev
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misc_feature
                                            misc_feature
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ORIGIN
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Direct Submission
Submitted (11-FEB-2000) Whitehead Institute/MIT Center for Genome Sebarith, 320 Charles Street, Cambridge, MA 02141, USA On MAy 25, 2000 this sequence version replaced g1:7139695, All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator B1g Dye; 100% of reads Assembly program: Phrap; version 0,960731 Consensus quality: 156445 bases at least Q40 Consensus quality: 165325 bases at least Q30 Consensus quality: 165395 bases at least Q20 Insert size: 173000; agarose-fp Insert size: 173000; agarose-fp Insert size: 166681; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 4.6 in 020 bases; agarose-fp Quality coverage: 4.8 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                               100 bp
of 1606 bp in length
100 bp
of 1714 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     536/

7120 719; app of 100 bp

7120 8211: contig of 1092 bp in length

8212 8311: gap of 100 bp

8312 9838: contig of 1547 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1746: contig of 1746 bp in length
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f 1653 bp in length
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9959 12581: contig of 2623 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17941 18040: gap of 100 bp
18041 21065: contig of 3025 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14: gap of 100 bp 27423: contig of 4009 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07: gap of 100 bp 38104: contig of 5497 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04: gap of 100 bp
43197: contig of 4993 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1747 1846: gap of 10
1847 3452: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5267 5366: gap of 10
5367 7019: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3453 3552: gap of 10
3553 5266: contig of
                                                                                                                                                                                                                                                                                                                                    Center clone name: 28_L_11
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48170: con+
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53635: cont
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15431: cont
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15532 17940; cont
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32508 32607:
32608 381
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43298 481
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117674. .136527

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117574 117673: gap of 100 bp 117674 136527: contig of 18854 bp in length 136528 136627: gap of 100 bp 136528 169181: contig of 32554 bp in length.
                                                                                             76616 76715: gap of 100 bp
76716 86772: contig of 10057 bp in length
86773 86872: gap of 100 bp
86873 99484: contig of 12612 bp in length
                                                                                                                                                                     99485 99584: gap of 100 bp
99585 117573: contig of 17989 bp in length
     60402 64778: contig of 4377 bp in length 64779 64878: gap of 100 bp 64879 69685: contig of 4807 bp in length
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Direct Submission
Submitted (12-SEP-1997) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
3 (bases 1 to 188741)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (03-FEB-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 188741)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS AC002542 188741 bp DNA DEFINITION Human BAC clone CTB-114A6 from 7q31, complete sequence.
ACCESSION AC002542
                                                                                2507 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davidson, S., Rohlfing, T., David, M. and Ahrens, C. The sequence of H. sapiens BAC clone CTB-114A6 Unpublished
                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: AC023303 from: 1 to: 169181
                                                                                                                                                                                                                                                     Percent Identity: 66.667
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Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                   between neighboring data submissions.
            ture //note="assembly_fragment"
136628. 169181
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46277 a 39522 c 38462 g 42413 t
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Center project name: H_RG114A06
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Waterston, R.
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4.091-
91.667
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08-881509-10 x AC023303/rev
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               The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send mailto:egreen@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                      NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP5-866N18. The actual start of
this clone is at base position 1 of CTB-114A6; actual end is at
188741 of CTB-114A6. This clone is part of an unanchored island,
                                                                                                                                                                                                                       This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 9785K. See: Shiruya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com).
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12714. .13075
700te="match to EST AA082591 (NID:g1624650) zn23h10.rl"
13159. .13302
700te="match to EST NS6179 (NID:g1199027)"
70pt_flamily="ll"
70pt_flamily="ll"
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/note="match to EST H65143 (NID:91023883) yu64c07.rl"
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/clone_lib="CITB-978SK-B"
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/db_xref="taxon:9606"
/chromosome="7"
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/rpt_family="ALU"
complement(11229. .11249)
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complement(19061, 19220
/rpt_family="ALU"
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12385, 19750
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14499. 1/700
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14873. .14945
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/rpt_family="ALU"
20495. .20538
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11804. .12114
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MAPPING INFORMATION:
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complement(25480...25620)
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36664. 37002
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complement(30271. .30330)
/rpt_family="L1"
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complement(31856. .31889)
/rpt_family="L1"
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complement(28075. .28106)
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complement(30633. 31188)
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complement(41783. .41819)
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24574. 2465
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'rpt_family="ALU"
/rpt_family="L1"
complement(20938.
/rpt_family="L1"
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36219. .36244
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3539. .23838
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complement(41704.
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34254. .34376
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/rpt_family="ALU"
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56166. .56187
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/rpt_family="L1"
56782. .56850
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                                                    3. .23198
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2887. 432
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55997. 561
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/rpt_family="L1"

08-881509-10.rge

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Kunst, F., Ogasawara, N. Moszer, I., Albertini, A. M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Brensia, M., Bragnel, S.C., Boriss, R., Bruschi, C. V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Enlich, S.D., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Enlich, S.D., Glaser, P., Goffeau, A., Golightly, E.J., Grandi, G., Guiseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwood, C.R., Henaut, A., Hilbert, H. Holsappel, S., Hosono, S., Hullo, M.F., Kalin, C., Kobayashi, Y., Koetter, P., Kohingstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Liu, H., Lardinois, S., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H., Lardinois, S., Mauel, C., Mediau, N., Mellado, R., Marina, S., Mauel, C., Medigue, C., Misulad, N., Mellado, R., Ogawa, K., Ogiwara, A., Oudega, B., Perscott, A.M., Prescean, E., Pulic, P., Portetelle, D., Porwollik, S., Nescott, A.M., Prescean, E., Pulic, P., Portetelle, D., Porwollik, S., Nescott, A.M., Prescean, E., Portetelle, D., Porwollik, S., Rose, M., Sadie, Y., Sato, T., Rivolta, C., Rocha, E., Roche, M., Sacho, S., Scolfone, F., Schleich, S., Scorto, P., Takahashi, H., Takamaru, K., Sorokin, A., Tanakoshi, A., Tanaka, T., Tarabisha, H., Weilers, Viari, A., Wambutt, R., Wedler, E., Wedeler, E., Wedeler, E., Wedeler, H., Weller, E., Weller, E., Weller, Weller, E., Vestikowa, H., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \frac{\text{BSUB0}\overline{0}10}{\text{Subtilis}} \frac{233780 \text{ bp}}{\text{subtilis}} \frac{\text{DNA}}{\text{complete genome (section 10 of 21): from 1781201}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The complete genome sequence of the gram-positive bacterium Bacillus subtilis
Nature 390 (6657), 249-256 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Kunst, F., Ogasawara, N., Yoshikawa, H. and Danchin, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                 Length: 12
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus/Staphylococcus group; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CysLeuValGlyArgSerAlaArgGlnLeuThrPhe 13
                                                                                                                                              /gene="WUGSC:H_RG114A06.1"
                                                                                    /rpt_family="ALU"
61071. .185981
                           /rpt_family="ALU"
59637. .59927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 233780)
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.57559
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Z99113.1 GI:2634090
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                                                                                                                                                                                                                                                                                      Ratio: 4.091
Percent Similarity: 91.667
                                                                                                                                                                                                                                                        45.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_ba2:BSUB0010
                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
08-881509-10 x AC002542
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Locus BSUB0010 2
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                                                                                                                                                                                                                                                              Quality:
   repeat_region
                                                                   repeat_region
                                                                                                                                                                                                                                   alignment_scores:
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TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
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/translation="WINEDLVEMESGOGSQYYHMGKELFKENTVFRQSMLEMDAIAARR IGTSIVEETYHPGKRVSDPFDSILFSHPAIFMITSYLKVKLEEDRGITPDYVGSVWEN SCOKGNALAILDRPQLINDHPQLFGNSELISINYDSHFVISGEEDHIRKIMEDLKEKG ILCQLLDPASTAFFSLIDPAGSAARFELDRAGSCHVMDENFW NAVRROMMFREAIRYLESQHTCKFIDLGPSGTLAMEVKQLIPGDSGTLAMEVKDITPFHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trānslation="MITYVFPGGSGKQGMGSGLFDEFKELTDQADEILGYSIKRLCL
ENPYSNLNKTQFTQPALYVVNALSYLKKIRDEEVKPDFVAGHSLGEYNALFAAEAFDF
ETGLQLVRKRGELMSLISNGGMAAVMGLNEEQVAKALKEYHLHDVDJANVNAPYQIVI
SGKKDEIEKAASLFETMTEVTWYLPLNVSGAFHSRYMNKAKEEFEEFLHAFYFSPPSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTLSELEAELKAVALTHSHYDHVNLVDPLTKMFNAQVYMSKKEIDYYQFRCRNLISL
DDHQTISIGNTRAQCLLTPGHTAGGMCYLFSESIFTGDTVFTEGCGICEDDGSSAEEM
FDSIQRIKSEVSPHVRVYPGHSFGKSPGHSIKDLYQHNIYFQIDKKEYFVKFRTRKNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALRHYFSTQDELLAFAMKLVQEKVTDRIKDIAVRDLLPKEKVLQILLEMVPTNRETIR
EMEVWFAFTAYARHKKDMFDASHDGIFSGMRNLIAYLDESDLLKQNADKDIEABRLYA
LVDGLALHAMLDPVRVNKDRIKRVIMQHVESICVEDTRETQKRHP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MPKQIDHEKRRKQIAEATWRVILERGMEGASARNIAKEAGLSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MNLTYKVHPIKTRYQGWTNYCYIIEDIVSRSAIVVDPSWELSKI
Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724
                      Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
                                                                                                                                                                                                                                                                                                            /function="regulation of the polyketide synthase operon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="involved in polyketide synthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="involved in polyketide synthesis"
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                                                                                                                                                                                                                                                                                                                                                                                                    /product="transcriptional regulator"
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/db_xref="G1:2634091"
                                                                                                                                                  /organism="Bacillus subtilis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SPTREMBL:034825"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:034381"
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                                                                                                                                                                                                  /db_xref="taxon:1423"
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                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/transl_table=11
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3302. /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="pksC"
1932. .2798
/gene="pksC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HRIKKDAEAMPR"
                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="pksD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="pksA"
                                                                                                                                                                                                                                               /gene="pksA"
75. .692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="pksB"
                                                                                                                                                                         /strain="168
                                                                                                                                                                                                                                                                                                  /gene="pksA"
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                                                                                                                 FEATURES
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gene

CDS

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HYWTLMTKPISVQEASEWGLIDAFDAESDVLLRKHLLRLRRLNKKGIAHYKQFMSSLD
HQVSRAKATALTANQDMFSDPQNQMGIIRYVETGQFPWEDQ"
10099-101848
10099. .10848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xue,Y., Wilson,D., Zhoo,L., Liu,Hw. and Sherman,D.H.
Hydroxylation of macrolactones YC-17 and narbomycin is mediated by
the pikC-encoded cytochrome P450 in Streptomyces venezuelae
Chem. Biol. 5 (11), 661-667 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firm.cutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 4342)
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Direct Submission
Submitted (17-JUL-1998) Department of Microbiology, University,
420 Delaware Street SE 1060, P.O. Box 196, Minneapolis, MN 55455,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="involved in the biosynthesis of macrolide antibiotics methymycin, neomethymycin, and pikromycin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xue,Y., Zhao,L., Liu,H.w. and Sherman,D.H.
A gene cluster for macrolide antibiotic biosynthesis in streptomyces venezuelae: architecture of metabolic diversity Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12111-12116 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Oct 28, 1998 this sequence version replaced gi:3777565.
Location/Qualifiers
1. .4342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF079139 4342 bp DNA BCT 28-OCT-
Streptomyces venezuelae pikCD operon, complete sequence.
AF079139
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/protein_id="AAC68886.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="cytochrome P450 monooxygenase"
                                                                                                                                                                                                                                                                           Quality: 45.00 Length: 13
Ratio: 3.462 Gaps Gaps Percent Similarity: 100.000 Percent Identity: 53.846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Streptomyces venezuelae"
/strain="ATCC15439"
/db xref="taxon:54571"
/db_xref="ATCC:15439"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44804 CACTGCTTTCTGGGCCAGTCCAAACAGCTTTCATTC 44842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TyrCysLeuValGlyArgSerAlaArgGlnLeuThrPhe 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 233780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: BSUB0010 from: 1
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/transl_table=11
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122. .1372
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08-881509-10 x BSUB0010
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VSINVYAEPYHQDRLKDTLSEOMDNWTVKWTDSIRFLMGRGEMEFAELGPGTVLTGLI
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                                                                                                                                                                      function="involved in polyketide synthesis"
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                                                                                                                                                                                                                                                           PMIRGLKALPIRWRRGREAGRRIG"
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H.sapiens mRNA for rearranged TCR junctional sequences x98410
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163066
166753
167277
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Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
                                         5.8e+03
5.9e+03
6.0e+03
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Schendel, D.J.
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                                                                                                                                seq_documentation_block:
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LOCUS HSTCRJUNC
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gb_htg19:AL139383
gb_p12:AP002866
gb_htg11:AC025318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Len | Documentation | 1341 | A93127 Sequence | from Patent | 1318 | X98410 H.Sapiens mRNA for rear | 36 | A93133 Sequence | from Patent EE | 39 | U30428 Human isolate M74 T-cell | 186797 | A0021965 Homo Sapiens clone | 506 | AF163060 Drechalera tritici-rep | 402 | L38878 Macaca mulatta (clone MN 995 | AL144658 Anopheles gamblae STS | 185286 | A0016721 Homo Sapiens chrome | 186787 | A007357 Homo Sapiens chrome | 195761 | A0018895 Homo Sapiens chrome | 1001814 | A0018805 | A0018805 | A0018805 | A0018805 | A0018805 | A0018805 | A
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AC069184 Homo sapiens chromos
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                                                               About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Database sequences: 1118133
Database length: -1736092196
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Query: 08-881509-1
                                                                                                              Command line parameters:
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gb_pr7:HSU27254
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gb_pr4:AR024739
gb_htg2:AL360012
gb_pl3:NCB15120
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gb_htg9:AC022514
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gb_htg17:AC073710
gb_sts2:G62404
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9b_pr7:HSU30448
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9b_htg17:AC073557
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gb_htg1:AC003059
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gb_htg16:AC069580
em_in:DMC001658
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9b_pr7:HSM800003
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9b_htg20:AL161942
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gb_pl2:AP001539
gb_tn1:AE003649
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AL1391061 Homo sapiens chr
AL139383 Homo sapiens chr
AP002866 Oryza sativa gen
AC025318 Homo sapiens chr
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YYCLVGGSARQLIFGSGTQLTVLPDIONPDPAVYQLROSKSSDKSVCLFTDEDSOTAV
YYCLVGGSARQLIFGSGTQLTVLPDIONPDPAVYQLROSKSSDKSVCLFTDEDSOTAV
SQSKDSDVYITDKTVLDMRSNDFKSNSAVAMSNKSDFACANAFNNSIIPEDTFFPSPE
SSCDVKLVEKSFETDTNLNFONLSVIGFRILLLKVAGFNLLMTLRLMSS"
55. 801
365 c 294 g 351 t
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J gene; junction; T cell receptor; TCR junctional sequence; V gene.
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Caternhini; Hominidae; Homo.
1 (bases 1 to 1318)
Jantzer, P.U. and Schendel, D.J.
Tumor-infiltrating lymphocytes recognizing spontaneously arising renal cell carcinomas express T cell receptors characteristic of a Unpublished
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source

FEATURES

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JOURNAL

R.T.P.T.T

REFERENCE AUTHORS 01-AUG-1995

08-881509-1.rge

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 39)
                                                                                                                                                                                                                                                                                              Human isolate M74.T-cell receptor alpha V-J junction (TCR Valpha 3/J alpha 22) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dave, V.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L. Restricted usage of T-cell receptor V alpha sequence and variable-joining pairs after normal T-cell development and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-JUN-1995) Julia L. Hurwitz, St. Jude Children's Research Hospital, Immunology, 332 N. Lauderdale, Memphls, TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="T-cell receptor alpha V-J junction"
/protein_id="AAA73607.1"
/db_xref="GI:915482"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 69:231
                                          Percent Identity: 83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="TCR Valpha 3/J alpha 22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="TCR Valpha 3/J alpha 22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunol. 37 (3), 178-184 (1993)
                                                                                                                                                                      2 CysLeuValGlyGlySerAlaArgGlnLeuThrPhe 13
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         Length:
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/isolate="M74"
                                                                                                                                 Align seg 1/1 to: A93139 from: 1 to: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
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VSGSARQLIFGXCLVGGSARQLIFGXCLAGSARQLIFGXCLAPSGSARQLIFGXC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JAN-2000
                                                        Submitted (11-JUN-1996) P. Jantzer, Institute for Immunology, Goethestr. 31, D- 80336 Munich, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 others
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                             /product="TCR junctional sequence"
/protein_id="CAA67057.1"
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                                                                                                                                                                                                                            /note="V gene/J gene junction"
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Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
                                                                                                                                                      /isolate="patients 22 and 26"
/db_xref="taxon:9606"
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                                                                                                                                   /organism="Homo sapiens"
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         2 (bases 1 to 1318)
Jantzer,P.
Direct Submission
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Ratio: 5.167
Percent Similarity: 100.000
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BASE COUNT ORIGIN

BASE COUNT ORIGIN

source

FEATURES

CDS

DEFINITION

ACCESSION

KEYWORDS

SOURCE

VERSION

ORGANISM

REFERENCE AUTHORS JOURNAL

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57572
85438
85538
                                                          JOURNAL.
                    AUTHORS
                                                                      REFERENCE
                                                                                                AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AC021965 186797 bp DNA HTG 04-APR-2000
DEFINITION HOMO Sapiens clone RP11-475J5, WORKING DRAFT SEQUENCE, 11 unordered
                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 39)
                              seq_documentation_block:
LOCUS HSU30448 39 bp mRNA PRI 01-AUG-1995
DEFINITION Human isolate M94 T-cell receptor alpha V-J junction (TCR Valpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 186797)
                                                                                                                                                                                                                                                           Dave, V.P., Larche, N., Rencher, S.D., Koop, B.F. and Hurwitz, J.L. Restricted usage of T-cell receptor V alpha sequence and variable-joining pairs after normal T-cell development and bone marrow transplantation
Hum. Immunol. 37 (3), 178-184 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-JUN-1995) Julia L. Hurwitz, St. Jude Children's Research Hospital, Immunology, 332 N. Lauderdale, Memphis, TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="T-cell receptor alpha V-J junction"
/protein_id="AAA73621.1"
/db_xref="G1:915516"
/translation="FCVSSGSARQLTF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="TCR Valpha 3/J alpha 22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="TCR Valpha 3/J alpha 22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TyrCysLeuValGlyGlySerAlaArgGlnLeuThrPhe 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TTCTGTGTCTCCTCTGGTTCTGCAAGGCAACTGACCTTT 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: HSU30448 from: 1 to: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /isolate="M94"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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AC021965.3 GI:7408035
HTG: HTGS_PHASE1; HTGS_DRAFT.
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9
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                                                                                                                                U30448.1 GI:915515
                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 39)
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Direct Submission
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seq_name: gb_pr7:HSU30448
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                                                                                                                                                                                    Homo saptens
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08-881509-1 x HSU30448
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                                                                                                                                                                                    ORGANISM
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TITLE
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Allen, B., Lintcon, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Bodess L. Co. 180/47).

Anderson, S., Baldwin, J., Barma, N., Beckerly, R., Beda, F., Bogualawkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Perreira, P., Fitzhugh, W., Forrest, C., Gaye, D., Galagan, J., Fatzhugh, W., Forrest, C., Gaye, D., Galagan, J., Farzhugh, W., Forrest, C., Gaye, D., Galagan, J., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Merwan, P., McGurk, A., McKernan, K., Norman, C. H., O'Connor, T., O'Connor, T., O'Oulvar, T., M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Ringe-Thomann, D., Stojanovic, N., Subramanlan, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Mu, X., Myman, D., Ye, W. J., Direct Submission and Zody, M., Talamas, J., Tesfaye, S., Theodore, J., Direct Submission and Sody, M., Viel, R., Vo, A., Mu, X., Wyman, D., Ye, W. J., Direct Submission and Sody, M., Stojanovic, N., Subramanlan, A., Talamas, J., Tesfaye, S., Theodore, J., Direct Submission and Sody, M., All repeats were identified using Repeatmasker:

Submitted (22-JAN-2000) Whitehead Institute/MIT Center for Genome On Apr 4, 2000 this sequence version replaced gl:6939487.

Smit, A. F. A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/Repeatmasker:html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
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* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence * as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator B19 Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 18146% bases at least 040 Consensus quality: 184129 bases at least 030 Consensus quality: 184946 bases at least 020 Insert size: 182000; agarose-fp Insert size: 185797; sum-of-contigs Quality coverage: 5.6 in Q20 bases; sum-of-contigs Quality coverage: 5.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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20838: contig of 5269 bp in length
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-475J5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- Project Information
ter project name: L6069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: 475_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name:
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                                                                                                     (bases 1 to 186797)
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                                                                       Unpublished
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/translation="MRQVARVIVELTLSTLSLAKTTOPISMDSYEGQEVNITCNHNDI
ATSDYIMWYQOFPOGEREIIQGYKANIANEVAŞLEIPTDRKSSTLSLPRVALSDTAV
YYCLVGDRYSGGSANRLIFGKGTHLIVQPYIQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alpha (TCR A) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wertebrata; Euteleostomi;
| Cercopithecidae;
2 (bases 1 to 506)
Goh,T.K. and Hyde,K.D.
Direct Submission
Submitted (28-JUN-1999), Ecology & Biodiversity, The University of
Hong Kong, Pokfulam Road, Hong Kong SAR; China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-JAN-1995
                                                                                                                                                                                                        /product="internal transcribed spacer 1"
                                                                                                                        /organism="Drechslera tritici-repentis"
                                                                                                                                                                                                                                                                                             /product="internal transcribed spacer 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macaca mulatta (clone MMVA165) T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="T-cell receptor alpha"
/protein_id="AAA60416.1"
/db_xref="G1:623133"
                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 90:00
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Mammalia, Eutheria, Primates, Catarrhini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Macaca mulatta TCR alpha chain sequences
Unpublished (1995)
                                                                                                                                                                                                                            183. .339
/product="5.8s ribosomal RNA"
                                                                                                                                                                                                                                                                                                                147 t
                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Macaca mulatta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AF163060 from: 1 to: 506
                                                                                                                                                           /db_xref="taxon:132100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 TGTTTACTTGGCGGGTCCGCCCCCATTG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CysLeuValGlyGlySerAlaArgGlnLeu 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9544"
/clone="MMVA165"
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                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                               115 g
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1 (bases 1 to 402)
                                                                                                                                         /strain="7819-1"
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                                                                                                                                                                                                                                                              340. .506
/note="ITS2"
                                                                                                                                                                                             /note="ITS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         402 bp
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L38878
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                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
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                                                                                                                                                                                  misc_RNA
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              REFERENCE
                              AUTHORS
                                                               JOURNAL
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                                                                                                 FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drechslera tritici-repentis.

Drechslera tritici-repentis

Drechslera tritici-repentis

Eukaryota: Fungi: Ascomycota: Pleosporaceae:
anamorphic Pleosporaceae: Drechslera.

1 (bases 1 to 506)

Goh,T.K. and Hyde,K.D.
Generic separation in the Helminthosporium-complex, based on sequence analysis of the rDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1011 others
                118262 118361: gap of 100 bp
118362 148993: contig of 30632 bp in length
148994 149093: gap of 100 bp
149094 186797: contig of 37704 bp in length.
                                                                                                                                                     /clone="RP11-475J5"
/clone_lib="RPCI-11 Human Male BAC"
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1 33479 c 31559 g 61128 t
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390. .11030
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                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION Anopheles gambiae STS SP6 end of clone 09C07 of Notrebamel library from strain PEST of Anopheles gambiae (African malaria mosquito), sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Petrygota; Neoptera; Endopterygota; Diptera; Nematocera;
Culicoidae; Culicidae; Anopheles.
1 (bases 1 to 995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J. Direct Submission
                                                                                                                                                                                                                                                1 TyrCysLeuVal......GlyGlySerAlaArgGlnLeuTh 12
                                                                                                              Percent Identity: 61.111
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222 c 216 g 269 t
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(bases 1 to 995)
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08-881509-1 x CNS01HNL/rev
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08-881509-1 x MACTCRAAT
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AC016721 185286 bp DNA HTG 07-JUL-2000
Homo sapiens chromosome 2 clone RP11-327J6, WORKING DRAFT SEQUENCE,
19 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 185286)
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On Mar 13, 2000 this sequence version replaced g1:7022633
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Center code: WUGSC
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1152: gap of unknown length
3846: contig of 2694 bp in length
3946: gap of unknown length
6182: contig of 2236 bp in length
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contig of 6653 bp in Length
gap of unknown length
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contig of 5345 bp in length
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1 TyrCysLeuValGlyGlySerAlaArgGlnLeuThrPhe 13
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HTG: HTGS_PHASE1; HTGS_DRAFT.
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Waterston, R.H.
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                                                                                                                                                                                                                                                                   seq_documentation_block:
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31653
311653
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gap of unknown length

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source. FEATURES

13

Length:

Quality: 47.00

BASE COUNT

ORIGIN

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Submitted (33-JUN-2000) Whitehead Institute/MIT Center for Genome Submitted (320 Charles Street, Cambridge, MA 02141, USA on Oct 4, 2000 this sequence version replaced gi:8671930.
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertehrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo. 1 (Dases 1 to 186787)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo. sapiens chromosome 2, clone RP11-70708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                     AC073557 186787 bp DNA HTG 04-OCT-2000 HTG 04-OCT-2000 HOMO Sapiens chromosome 2 clone RP11-70708 map 2, WORKING DRAFT SEQUENCE, 30 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: 707_0_8

Center clone name: 707_0_8

Sequencing vector: M13 M77815; 100% of reads Sequencing vector: M13 M77815; 100% of read Assembly program: Phrap; version 0.956731

Consensus quality: 172755 bases at least 040

Consensus quality: 173967 bases at least 030

Consensus quality: 182697 bases at least 030
                                                                                                    185286
             Percent Identity: 53.846
                                                                                                                                                             Align seg 1/1 to reverse of: AC016721 from: 1 to;
                                                                                                                                       1 TyrCysLeuValGlyGlySerAlaArgGlnLeuThrPhe 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- Genome Center
                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name:
                                                                                                                                                                                                                                                                                                                                       AC073557.2 GI:10567944
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3.917
92.308
                                                     alignment_block:
08-881509-1 x AC016721/rev
                                                                                                                                                                                                               seq_name: gb_htg17:AC073557
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LOCUS AC073557 1
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 Ratio:
Percent Similarity:
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KEYWORDS
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source
                                                                                                                                                                                                                                                                                                     arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
Insert size: 192000; agarose-fp
Insert size: 183887; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; agarose-fp
Quality coverage: 4.4 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              654 6753: gap of 100 bp 6754 8306: contig of 1553 bp in length 8307 8406: gap of 100 bp 73483 32582: contig of 24076 bp in length 32583: gap of 100 bp 73583 33576: contig of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3076 3175; gap of 100 bp 3176 4344; contig of 1169 bp in length 4445 5456; contig of 100 bp 1
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34786: contig of 1010 bp in length
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47249: gap of 100 bp in length
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42255 156210: contig of 13956 bp in length
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56311 169999: cont1g of 13689 bp in length
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70100 185820: contig of 15721 bp in length
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185921 186787: contig of 867 bp in length.
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40126: conf
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43734 47149; conf
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60061: cont
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64006: cont
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FEATURES

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5: gap of unknown length
1: contig of 16786 bp in length
1: gap of unknown length
9: contig of 14608 bp in length
9: gap of unknown length
1: contig of 22332 bp in length
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gap of unknown length
contig of 8024 bp in length
gap of unknown length
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of 8509 bp in length
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of 5380
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                17105:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (21-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
On Aug 12, 2000 this sequence version replaced gi:7658490.
                                                                                                                                                                                                   AC018895 195761 bp DNA HTG 12-AUG-2000
Homo sapiens chromosome 5 clone RP11-569B5, WORKING DRAFT SEQUENCE,
27 unordered pieces.
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                             12-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1562: contig of 1562 bp in length
1662: gap of unknown length
4370: contig of 2708 bp in length
4470: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of unknown length
contig of 3993 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 2445 bp in length
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unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown length
                                                                                                                Percent Identity: 53.846
                                                                                                1 TyrCysLeuValGlyGlySerAlaArgGlnLeuThrPhe 13
                                                                   Align seg 1/1 to: AC073557 from: 1 to: 186787
                                                                                                                                                                                                                                                                                                                                                                The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                        AC018895.3 GI:9798023
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                              (bases 1 to 195761)
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7015:
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 Percent Similarity: 92.308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved.
                                                                                                                                                           seq_name: gb_htg7:AC018895
                                                                                                                                                                                                                                                                                                                                                           Waterston, R.H.
                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                      seq_documentation_block:
                                 alignment_block:
08-881509-1 x AC073557
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                                                                                                                                                                                                                                             AC018895
                                                                                                                                                                                                                                                                                          human.
                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                        ORGANISM
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REFERENCE AUTHORS

TITLE

ACCESSION VERSION

SOURCE

JOURNAL

TITLE

COMMENT

AUTHORS JOURNAL REFERENCE

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HSM800003 1492 bp mRNA PRI 18-FEB-2000 HOMO sapiens mRNA; cDNA DKFZp56411916 (from clone DKFZp56411916).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Martinsried, GERWANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Koehrer,K., Beyer A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1492)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2607 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: AC018895 from: 1 to: 195761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 61.538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122675 TATTGCTTACTTGTGGTGGGGAGAAACTCCTCACATTT 122637
           39185, .44564
/note="assembly_name:Contig21"
                                             44665. .50380
/note="assembly_name:Contig22"
                                                                                 50481. 58039 _______/note="assembly_name:Contig23"
                                                                                                                                                                  ა4ააა. ,/საჯა
/note="assembly_name:Contig25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            118348. 130090
//note="assembly_name:Contig32"
130191. 141735
/note="assembly_name:Contig33"
141836. 158621
                                                                                                                                      /note="assembly_name:Contig24"
                                                                                                                                                                                          71094, 78868 - 7004-"assembly_name:Contig26" 78969, 85138 / 70ce-"assembly_name:Contig27
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/note="assembly_name:Contig29"
                                                                                                                                                                                                                                                                                                                                                                                       99595. .108103
/note="assembly_name:Contig30"
108204. .118247
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig34"
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173430. .195761
                                                                                                                                                                                                                                                                                                         85239. . . 93262
/note="assembly_name:Contig28"
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a 33956 c 35611 g 62640 t
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vector_side:right"
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Percent Similarity: 84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
08-881509-1 x AC018895/rev
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ALECT SUBMINISTATION

SUBMITTED (19-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CBLO 15A, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequestReanger.ac.uk

On Jul 7, 2000 this sequence version replaced gi:7940159.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences with an all overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the feature feature feature is an annotation using the 'unsure'
                                                            This clone (DKFZp56411916) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://www.mips.biochem.mpg.de/proj/cDNA/.
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSDJ22II7 86654 bp DNA PRI 24-JUL-2000 Human DNA sequence from clone RPI-22II7 on chromosome 6q11.1-12. Contains the 3' end of the gene KIAA0244, the 3' end of the gene FIAA0245, the 3' end of the gene for a novel protein with EGF-like and laminin G domains, ESTS, STSS and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 86654)

                                                                                                                                                                                                                                                                                                                            /clone="DKFZpS641996"
/clone_ib==564 (synonym: hfbr2). Vector pAMP1; host
/dev_stage="fetal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; EGF-like domain; KIAA0244; laminin G domain.
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Gaps: 0
Percent Identity: 66.667
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                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="brain"
1456. .1461
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AL050329.12 GI:8977876
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Percent Similarity: 91.667
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                                     Genome Project
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KEYWORDS
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http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                                                                 Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1145. .4266
note="LIMA8 repeat: matches 6146. .6284 of consensus"
                                                                                                           http://www.sanger.ac.uk/HGP/Chr6
RPI-22117 is from the library RPCI-1 constructed at the Roswell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2294. 2744
horte="nigger2a repeat: matches 1. .434 of consensus"
3264. 3407
hote="72 copies 2 mer tt 57% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    679. .3721
'note="MLT2FB repeat: matches 367. .405 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5681. .6116
/note="LTR40b repeat: matches 25. .459 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Alusx repeat: matches 23. .296 of consensus"
12030. .12143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3777. .4144
/note="MLT2FB repeat: matches 4. .365 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="L2 repeat: matches 2587. .2692 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="AluJb repeat: matches 113. .197 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 812. 946
//note="FLAM_C repeat: matches 1. .133 of consensus"
complement(1059. .1556)
complement(1634. .2230)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1598. .4822
/note="MER46A repeat: matches 1. .236 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MLT1J repeat: matches 8. .515 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .798 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5898. .7228
/note="MER1B repeat: matches 1. .337 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="AluSx repeat: matches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="AluSp repeat: matches 1. .288 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="AluJb repeat: matches 1. .113 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="MER2 repeat: matches 2. .256 of consensus"
1756. .12029
                                                                                                                                                                                                                        This sequence is the entire insert of clone RP1-22117.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3722. .3757
/note="18 copies 2 mer gt 100% conserved"
                                                                                   Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1755. .2079
/note="HAL1 repeat: matches 458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(8541. .9047)
/note="match: GSS: Em:AQ883741"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9071. .9568
//note="match: GSS: Em:AQ677335"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: GSS: Em:AQ814479"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(1634. .2230)
/note="match: GSS: Em:AQ321324"
1755. .2079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1772. .2228)
/note="match: GSS: Em:AQ772565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(6311. .6453)
/note="match: STS: Em:G35019"
on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP1-22117"
/clone_lib="RPCI-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(6311.
                                                                                                                                                                                                                                                                                                                                                                /map="q11.1-12"
                                                                                                                                                                                                                                                                                                                                          /chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .10788
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                                                                                                                                                                                                                                                                             .86654
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                                                                                                                                                                                                          VECTOR: pCYPAC2
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match: ESTS: Em:AA7479114 Em:AA677675 Em:AA768938
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Em:AA312781 Em:AA735379 Em:AN184930 Em:AA18757
Em:AA312781 Em:AA133838 Em:AW649607 Em:AA18757
Em:AA018594 Em:AA133838 Em:AW609578 Em:AA789461 Em:AA133511
Em:Z1347 Em:AA32675 Em:AA786465 Em:AA789461 Em:AA2186
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Em:AR86958 Em:AA8864 Em:BA14478 Em:AT41078 Em:E01314
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Em:AA3381 Em:AA56744 Em:AA86120 Em:R8349
Em:AA3381 Em:AA56744 Em:AA86599 Em:R8349
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                                                                                                                                                                   13064. 13192
/note="LlMC/D repeat: matches 5728. 5868 of consensus"
13348. 13639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12524. .12704
/note="L1MC5_repeat: matches 7510. .7707 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="AluSc repeat: matches 51. .299 of consensus"
16995. .17140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="12 repeat: matches 2367. .2525 of consensus"
16745. .16994
                                                                                                                                                                                                                                                                                                                                                                         16245. .16346
//note="L2 repeat: matches 2639. .2745 of consensus"
16356. .16434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6995. 17140
hoote="AluSc repeat: matches 1. .146 of consensus"
                                                                                                                                                                                                                                                                        /note="AluJb repeat: matches 1. .290 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WADE1 repeat: matches 1. .79 of consensus" .16635
                                                                                                                                                                                                                                                                                                                                                            /note="Alur repeat: matches 2. .311 of consensus"
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/product="dJ22117.1 (KIAA0244)"
25320, .25395
12333. .12747
/note="match: GSS: Em:AQ006173"
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Submitted (29-JUN-2000) Sanger Centre, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 1, 2000 this sequence version replaced gi:8546598.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations variation anotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with This sequence has been finished according to sequence as with This sequence has been finished according to sequence as we submit sequences with This sequence has been finished according to sequence as we submit sequences with This sequence has been finished according to sequence as we submit sequences with This sequence has been finished according to sequence as we submit sequences with This sequence has been finished according to sequence as we submit sequences with This sequence has been finished according to sequence as we submit sequences with the sequence has been finished according to sequence as we submit sequences with the sequence has been finished according to sequence as we submit sequences with the sequence as sequence as we submit sequences with the sequence as sequences as we submit sequences as the sequence as sequences are sequences as the sequence as sequences are sequences sequenc
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Human DNA sequence from clone RP11-40A8 on chromosome 13, complete
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5325. 53314
forced join. Digest suggests there may be 200bp missing
from the tandem repeat."
/note="HAL1 repeat: matches 1551. .1627 of consensus" 25399. .25428
/note="15 copies 2 mer tt 90% conserved" 25782. .26672
                                                                                                                               15782. .26672
/note="HAL1 repeat: matches 147. .1094 of consensus"
                                                                                                                                                                                               'note="AluY repeat: matches 83, .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="54 copies 2 mer cc 75% conserved"
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Ratio: 3.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 58.333
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08-881509-1 x HSDJ22I17
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LOCUS AL137881 1.
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP, Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'

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This sequence is the entire insert of clone RP11-40A8 The true left end of clone RP11-547C18 is at 69479 in this sequence. The true right end of clone RP11-233H19 is at 14112 in this sequence.
chromosome 13, constructed by the Sanger Centre Chromosome 13 mapping Group. Further information can be found at http://www.sanger.ac.uh/HGP/Chr13 RP11-40A8 is from the library RCI-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                      4.182 Gaps: 0
91.667 Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AL137881 from: 1 to: 143324
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                                                                                                                                                                                                                                         1. 143324
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                        /chromosome="13"
/clone="RP11-40A8"
/clone_lib="RPCI-11.1"
19526. .19591
                                                                                                                                                                                                                       Location/Qualifiers
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Page 12

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i AF127771 Homo sapiens cell-
i X66604 Pseudomonas sp. plas
i AE000662 Homo sapiens T-ce
i M94081 Human Tcr-C-delta g
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Jantzer, P.U. and Schendel, D.J.
Tumor-infiltrating lymphocytes recognizing spontaneously arising renal cell carcinomas express T cell receptors characteristic of a
                                                                                                                                                                                                                                                  22-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutherla;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission Submitset (11-JUN-1996) P. Jantzer, Institute for Immunology, Goethestr. 31, D- 80336 Munich, FRG Locátion/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSTCRJUNC 1318 bp mRNA PRI 08-JA
H.sapiens mRNA for rearranged TCR junctional sequences
X98410
                                      4091 1
8280 1
71153
97630
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Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                          unidentified
unclassified.
1 (bases 1 to 39)
Schedl, D.J.
T-cells specific for kidney carcinoma
Patent: EP 0816496-A 07-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAB69531.1"
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                                   70.53
145.83
1.3e+03
1.9e+03
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Sequence 5 from Patent EP0816496.

    .39
    /organism="unidentified"

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                                                                                                                                                                                                                                                                                                                   A93131.1 GI:6741520
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Percent Similarity: 100.000
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LOCUS
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                             gb_pr3:AF127771
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gb_pr7:HUAE000662
                                                                                                          gb_pr8:HUMTCRADCV
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AC069515 Homo sapiens chrome
AC036168 Homo sapiens chrome
AC019062 Homo sapiens chrome
AC017084 Homo sapiens chrome
AC059255 Homo sapiens chrome
                                                                                                                                                                                                 -WODEL-Frame+p2n.model -DEV-xlp
-Q=/Cgn2_1/USPTO_spool/DECLOUX-08-881509/runat_28032001_092236_29744/app_query.fasta_l.
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183 | M17666 Human T-cell receptor ad
69627 | AL035424 Himan Tuna
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502 : AC013738 Homo sapiens chromc
1 U30448 Human isolate M94 T-cell
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X02886 Human gene for T-cell re
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AC022407
                                                                                                       About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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OM of: 08-881509-2 to: GenEmbl:* out_format : pfs
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Database sequences: 1118133
Database length: -1736092196
Search time (sec): 3669.890000
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Query length: 14
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gb_htg5:AC016140
gb_htg11:AC025530
gb_pr3:AC009319
gb_htg14:AC048347
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9b_hr98:AC013738
9b_hr98:AC01752
9b_hr99:AC022407
9b_hr99:AC022407
9b_hr916:AC025515
9b_hr917:AC056168
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gb_pr6:HSA235208
gb_pr8:S69140
gb_pat1:A93127
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gb_pr7:HSU27254
gb_in1:AE003100
gb_ro:AC003694
gb_pr8:HUMTCAZA
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gb_htg16:AC069255
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9b_pr8:HUMTCRACG
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gb_pr3:AF043892
gb_pr3:AF043894
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gb_pr3:AF043876
gb_pr3:AF043877
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gb_sts1:G48903
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alignment_scores:
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BASE COUNT
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                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (15-OCT-1998) Cross S.M., Queensland Institute of Medical Research, The Bancroft Centre, 300 Herston Road, Brisbane,
                                                                                                                                                                                                                                                                             TGSARQITFGXCLVGGDTDKLIFGXCLVLSGSARQLFFGXCLVLSGSARQLFFGXCLV
VSGSARQLTFGXCLALGGSARQLFFGXCLALAGSARQLTFGXCLAFSGSARQLTFGXC
LVAGGGNTPLVFGXCLVGSARQLFFGXCLVGSARQLTFGXXLVGRSARQLTFGXCL
ATGSARQLTFGXCLVGAGGYQKVTFGXCLVLSGSARQLTFGXCLVAPCGATNKLIFGX
CLVVLGGSQGNLIFGXCLVGPNNAGNMLTFGXCLVATNQGRNCSDLW"
329 c 352 g 344 t 87 others
                                                                                                                                                                                                                                         LVLSGSARQLTFGXCLVLSGSARQLTFGXCLVGGSARQLTFGXCLVGGSARQLTFGXC
LVSGSARQLTFGXCLDSGSARQLTFGXCLDSGSARQLTFGXCLPSGSARQLTFGXCLA
                                                                                                                                                                                                                   /translation="CLVGGSARQLTFGXCLATGSARQLTFGXCLVLSGSARQLTFGXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSAZ35208 42 bp mRNA PRI 12-MAR-1999
Homo sapiens mRNA for T cell receptor alpha chain V-J junctional
region (TCRAV7AJ16S3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crossreactive recognition of viral, self, and bacterial peptide ligands by human class I-restricted cytotoxic I lymphocyte clonotypes: implications for molecular mimicry in autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #A235208.1 GI:3851223
T cell receptor; T cell receptor alpha chain; variable region
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Misko,I.S., Cross,S.M., Khanna,R., Elliott,S.L., Schmidt,C.,
Pye,S.J. and Silins,S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 96 (5), 2279-2284 (1999)
99162595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 100.000
                                                                                                                                                       /product="TCR junctional sequence"
/protein_id="CAA67057.1"
/db_xref="G1:1770561"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CysLeuValLeuSerGlySerAlaArgGlnLeuThrPhe 14
                                                                                                                 /note="V gene/J gene junction"
/codon_start=1
                            /isolate="patients 22 and 26"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: HSTCRJUNC from: 1 to: 1318
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/db_xref="taxon:9606"
             /organism="Homo sapiens"
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio: 4.923
Percent Similarity: 100.000
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LOCUS HSA235208
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SOURCE

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Maggi, E. and Romagnani, S. Molecular basis of cross-reactivity among allergen-specific human T Molecular basis of cross-reactivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS S69140 98 bp mRNA PRI 23-SEP-1994 DEFINITION TCR V alpha=T-cell receptor alpha-chain (allergen-specific) [human, grass.sensitive individual VI 19, peripheral blood, mRNA Partial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="This sequence comes from Fig. 3b; Protein sequence is in conflict with the conceptual translation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 98)
Mohapatra, S.S., Mohapatra, S., Yang, M., Ansari, A.A., Parronchi, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells: T-cell receptor V alpha gene usage and epitope structure Immunology 81 (1), 15-20 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genbank staff at the National Library of Medicine created this entry [NCBI gibbsq 144562] from the original journal article. This sequence comes from Fig. 3a. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /exception="Protein longer than coding region shown;
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/product="T-cell receptor alpha-chain"
/protein_id="Anaba244.1"
/db_xref="G1:545974"
/translation="DSATYFCAALPESARQLTFGSGTQLTVLPDIQN"
a 27 c 20 g 28 t
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/note="T-cell receptor alpha-chain"
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                                                                                                                                                 Length: 13
Gaps: 0
Percent Identity: 84.615
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/db_xref="taxon:9606"
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/cell_line="SP1"
1. .42
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08-881509-2 x HSA235208
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Treell receptor usage by anti-melanoma specific cytotoxic tumor-infiltrating lymphocytes. Detection of dominant tumor-specific Treell clones by single strand conformational polymorphism and Treell clones by single strand conformational Unpublished (1995)

E. Ubases I to 214)

S. Kurnick, J. T., Ihara, A., Pervaiz, S., Pandolfi, F., Van, Den Elsen P., Waitkus, R., Boyle, L.A., Hishii, M. and Andrews, D.M.

L. Submitted (16-NOV-1995) James T. Kurnick, Pathology Research Laboratory, Massachusetts General Hospital, 149 East 13 St., Charlestown, MA 02129, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 87)
Yandevyver,C., Mertens,N., van den Elsen,P., Medaer,R., Raus,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   patients with multiple sclerosis: restricted T cell receptor V gene rearrangements and CDR3 sequence
Eur. J. Immunol. 25 (4), 958-968 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMTCRACG 87 bp mRNA PRI 07-NOV-1995
Homo sapiens (clone NS1-F4) T cell receptor alpha chaln (TCRA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clonal expansion of myelin basic protein-reactive T cells in
                          Waitkus, R., Boyle, L.A., Hishii, M. and Andrews, D.M.
                                                                                                                                                                                                                                                                                                                                                                        /clone="WU 57"
/cell_type="cytotoxic T-cell lymphocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product-"T-cell receptor alpha chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.00 Length: 13
4.727 Gaps: 0
84.615 Percent Identity: 84.615
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L42801.1 GI:853662
T cell receptor alpha.
Homo sapiens (clone: NS1-F4) cDNA to mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CysLeuValLeuSerGlySerAlaArgGlnLeuThrPhe 14
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Ratio:
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JOURNAL
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                                                                                                                       JOURNAL
                                                                                                                                                                   AUTHORS
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AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /Translation="MROVARVIVELFLSTLSIARTHOPISMDSYEGDEVNITCSHNNI
TYDVITHOOFPSGEPRFIIGSKTRVTNEVASLFIPADRKSSTLSLPRVSLSDTAV
YYCLVGGSARQLFGSGTQTVLPDIONPDPAVYOLGNSKSSSDSWCLFTDFDSOTNV
SQSKDSOVITHORTLDMRSMDFKSNBAVAMSNKSDFACANAFNNSIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human T-cell receptor alpha chain (TCRAV281J22) mRNA, partial cds. U40776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 214)
Kurnick,J.T., Ihara,A., Perváiz,S., Pandolfi,F., Van,Den Elsen P.,
                                                                                                                                                                                                                                                              22-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1995
                                                                                                                                                                                                                                                            PAT
                                                                                                      1 TyrCysLeuValLeuSerGlySerAlaArgGlnLeuThrPhe 14
                                                                                                                              310 TACTGCCTCGTG...GGTGGTTCTGCAAGGCAACTGACCTTT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 1
Percent Identity: 85.714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 1341)
Schendel, D. J.
T-cells specific for kidney carcinoma Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 t
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/protein_id="CAB69529.1"
/db_xref="G1:6741517"
                                                                                                                                                                                                                                                 LOCUS A93127 1341 bp DNA DEFINITION Sequence 1 from Patent EP0816496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: A93127 from: 1 to: 1341
                                                               to: S69140 from: 1 to: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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4.038
92.857
                                                                                                                                                                                                                             seq_documentation_block:
LOCUS A93127
                                                                                                                                                                                                                                                                                                                                                                             unidentified unclassified.
                                                                                                                                                                                      seq_name: gb_pat1:A93127
                                                                                                                                                                                                                                                                                                                                                         unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_pr7:HSU40776
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                       08-881509-2 x S69140
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08-881509-2 x A93127
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Percent Similarity:
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                                                               Align seg 1/1
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DEFINITION

ACCESSION

KEYWORDS VERSION SOURCE ORGANISM

AUTHORS REFERENCE

source

ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

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KEYWORDS

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alignment_scores:
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                                                     ORIGIN
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/product="T_c=11 receptor variable alpha chain"
/protein_id="AAB2021.1"
/protein_id="AB2021.1"
/protein_id="AB2021.1"
/protein_id="AB2021.1"
/protein_id="AB2021.1"
/protein_id="AB2021.1"
/product="T_c=1"
/product=
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 716)
Griesinger, F., Jansen, B. and Kersey, J. H.
Differentiation in mature T lymphoid leukemia cells is unstable and reversible to myeloid cells, without the involvement of a common stem cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S63879 716 bp DNA PRI 04-MAY-2000
TCR V alpha =T cell receptor variable alpha chain [human, MT-ALL,
Genomic Mutant, 716 nt].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenBank staff at the National Library of Medicine created this entry [NCBI glabsq 63879] from the original journal article. This sequence comes from Figure 4.

Location/Qualifiers
                                                                                                                                                      (19. .75), partial TCRCA (76. .87)" (16. .18), TCRJA (20. .75), partial TCRCA (76. .87)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                   /product="T cell receptor alpha chain"
/protein_id="AAA80964.1"
/db_xref="G1:853663"
/translation="YFCAEASGSARQLIFGSGTQLTVLPDIQK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Consility: 51.00 Length: 14 Ratio: 4.636 Gaps: 0 Percent Similarity: 78.571 Percent Identity: 71.429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TyrCysLeuValLeuSerGlySerAlaArgGlnLeuThrPhe 14
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/note="TCR V&agr"
join(58. .109,340. .>716)
/gene="TCR V alpha"
                                                                                                                                                                                                                                                                                                                    /db_xref="GDB:G00-120-404"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: HUMTCRACG from: 1 to: 87
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/db_xref="taxon:9606"
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/clone="NS1-F4"
                              /map="14q11.2"
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                                                                                                           "TCRA"
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                                                                                                                                              .>87
                                                                     .87
                                                                                                                   /gene=
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MEDLINE
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/note="Contains the 3' end of the TCRAV/TCRBV, the nDn/n, and the 5' end of the TCRAJ/TCRBJ."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS AF043888 51 bp mRNA PRI 11-NOV-1998
DEFINITION Homo sapiens patient CS-1 clone AV228 T cell receptor alpha chain CDR3 (TCRA) mRNA, partial cds.
ACCESSION AF043888.1 GI:3859395
VERSION AF043888.1 GI:3859395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 51)

Striebich, C.C., Falta, M.T., Wang, Y., Bill, J. and Kotzin, B.L.
Selective accumulation of related CD4+ T cell clones in the synovial fluid of patients with rheumatoid arthritis

J. Immunol. 161 (8), 4428-4436 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="from rheumatoid arthritis patient CS-1 [TCRAV1S3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (21.JAN-1998) Pediatrics, National Jewish Medical and Research Center, 1400 Jackson St., Denver, CO 80206, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 51)
Striebich,C.C., Falta,M.T., Wang,Y., Bill,J. and Kotzin,B.L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="T_cell receptor alpha chain CDR3"
/protein_id="AAC72683.1"
/db_xref="G1:3859396"
/translation="xFCAVRISSARQLTFG"
/translation="xFCAVRISSARQLTFG"
YSGTYFCGTASGSARQLTFGSGTQLTVLPDIQNPDPAVYQL"
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Percent Identity: 73.333
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                                                                                                                                                                                     Percent Identity: 71.429
                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="synovial fluid"
/clone="AV228"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                         Length:
                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                               Align seg 1/1 to: S63879 from: 1 to: 716
                             177 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="TCRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="TCRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [TCRAJ22]"
                             159 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.808
                                                                                                                                                               4.167
                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_pr3:AF043888
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08-881509-2 x AF043888
                               197 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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                                                                                                                                                                                                                                        alignment_block: 08-881509-2 x S63879
                                                                                                                                                 Quality:
Ratio:
                                                                                                                                                                                          Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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DEFINITION

ACCESSION KEYWORDS

VERSION

ORGANISM

AUTHORS TITLE

MEDLINE JOURNAL

AUTHORS REFERENCE

JOURNAL FEATURES

REFERENCE

S

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Direct Submission
Submitted (17-MAY-1995) Julia L. Hurwitz, Immunology, St. Jude
Children's Research Hospital, 332 N. Lauderdale, Memphis, TN 38101,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazora: Arthropoda: Tracheata: Hexapoda: Insecta; Pterygota: Metazora: Arthropoda: Tracheata: Brachveera; Pterygota: Neoptera: Endopterygota: Diptera: Brachveera; Muscomorpha: Ephydroidea: Drosophilidae; Drosophila.

1 (bases 1 to 6822)
Adams.M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., Gorgoe, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D., Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Miklos, G.L., Abril, J.F., Agbayani, A., An, H.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE003100 68222 bp DNA INV 06-0CT-2000
Drosophila melanogaster genomic scaffold 142000013385418, complete
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                   1 (bases 1 to 48)
Dave, V.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L.
Restricted usage of T-cell receptor V alpha sequence and variable-joining pairs after normal T-cell development and bone marrow transplantation
Hum. Immunol. 37 (3), 178-184 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="encodes V alpha 5/J alpha 22 junction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="T-cell receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: HSU27254 from: 1 to: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 CTCCTATCTGGTTCTGCAAGGCAACTGACCTTT 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 ValLeuSerGlySerAlaArgGlnLeuThrPhe 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /evidence-experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /isolate="M30"
/db_xref="taxon:9606"
/tissue_type="blood"
<1..>48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68222 bp
                                              U27254.1 GI:857594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 c
  mRNA, partial cds.
U27254
                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 4.364
Percent Similarity: 100.000
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                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
08-881509-2 x HSU27254
                                                                                                                                                                                                                                                                                                                                                                        Hurwitz, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
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                                                                                                                                                                                                                                                                                                                               94064390
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                                                                                               human.
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                                                                                        SOURCE
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                        ACCESSION
                                                                                                                                                                                                         AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                    KEYWORDS
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                                              VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="from rheumatoid arthritis patient CS-1 [TCRAV16S1]
                                                                                                                                                                                                                AF043886 51 bp mRNA PRI 11-NOV-1998
Homo sapiens patient CS-1 clone AV314 T cell receptor alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Contains the 3' end of the TCRAV/TCRBV, the nDn/n, and the 5' end of the TCRAJ/TCRBJ."
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-7AN-1998) Pediatrics, National Jewish Medical and Research Center, 1400 Jackson St., Denver, CO 80206, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seg_documentation_block:
LOCUS HSU27254 48 bp mRNA PRI 10-JUN-1995
DEFINITION Human isolate M30 T-cell receptor V-alpha 5/J alpha 22 junction
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 51)
Strieblich (C.C., Falta M.T., Wang,Y., Bill,J. and Kotzin,B.L. Selective accumulation of related CD4+ T cell clones in the synovial fluid of patients with rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 51)
Striebich,C.C., Falta,M.T., Wang,Y., Bill,J. and Kotzin,B.L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="T cell receptor alpha chain CDR3"
                                                 1 TyrCysLeuVal...LeuSerGlySerAlaArgGlnLeuThrPhe 14
                                                                       1 TyrCysLeuVal...LeuSerGlySerAlaArgGlnLeuThrPhe 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity: 86.667 Percent Identity: 73.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="YFCAVRLTGSARQLTFG"
11 c 13 g 17 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="synovial fluid"
/clone="AV314"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
            to: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAC72681.1"
/db_xref="G1:3859392"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AF043886 from: 1 to: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606
Align seg 1/1 to: AF043888 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                      AF043886.1 GI:3859391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="TCRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="TCRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . >51
                                                                                                                                              seg_name: gb_pr3:AF043886
                                                                                                                                                                                     seq_documentation_block:
LOCUS AF043886
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_pr7:HSU27254
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                                                                                                                                                                                                                                                                                                                                                       human,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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source

gene

BASE COUNT ORIGIN

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Andrews-Pfannkcoh, C., Baldwin, D., Baalew, R. M., Basu, A.,
Baxendale, J., Bayraktaroglu, L., Beasley, E. M., Beeson, K.Y.,
Baxendale, J., Bayraktaroglu, L., Beasley, E. M., Beeson, K.Y.,
Botchan, M. R., Bouck, J., Brokstein, P., Brotlier, P., Burtis, K.C.,
Busam, D.A., Butler, H., Cadieu, E., Center, A., Chandral. I.
Cherry, J. M., Cawley, S., Dahlke, C., Davenport, L. B., Davies, P., Gabrier, A., Deng, L. D., Dew, I., Dietz, S. M.,
Dodson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dunkov, B.,
Fleischmann, W., Fosler, C., Gabriellan, E., Gorrell, J. H., Gu, Z.,
Guan, P., Harris, M., Harris, N. L., Harvey, D., Helman, T. J.,
Hernandez, J. R., Houck, J., Hostin, D., Houston, K. A., Howalman, W., Galser, K., Glodek, A., Gong, F., Gorrell, J. H., Gu, Z.,
Gelbart, W. M., Glasser, K., Glodek, A., Gong, F., Gorrell, J. H., Gu, Z.,
Kennison, D. A., Ketchum, K. A., Kimmel, B. E., Kodira, C. D., Kraft, C.,
Kravitz, S., Kulp, D., Lali, Z., Lasky, P., Lei, Y., Lei, Y., Mattel, B., McIntosh, T. C.,
Ii, J., Li, Z., Liang, Y., Lin, X., Liu, X., Mattel, B., McIntosh, T. C.,
McIeod, M. P., McPherson, D., Merkulov, G., Milshina, N. V., Mobarry, C.,
Muzny, D. M., Nelson, D.L., Nelson, K. A., Nixon, K.,
Nusskern, D.R., Pecleb, J. M., Palazzolo, M., Pittman, G.S., Pan, Simpson, M., Schoeler, F., Shen, H., Shue, B.C., Siden Kiamos, I.,
Saunders, R. D., Schoeler, F., Shen, H., Shue, B.C., Siden Kiamos, I.,
Saunders, R. D., Schoeler, F., Sanith, T., Shue, B.C., Stanington, K.,
Sthopski, M., Weissenbach, J., Wallians, S. M., Woodage, T.,
Weinstock, G. M., Weissenbach, J., Wallians, S. M., Woodage, T.,
Weinstock, G. M., Weissenbach, J., Wollians, S. M., Woodage, T.,
Weinstock, G. M., Weissenbach, J., Shue, S., Zhuy, X., Smith, H.O.,
Glbbs, R. A., Myers, E.W., Rubhi, G. M. and Venter, J. C.,
The genome sequence of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MYRDRWRTGKRWTGPHIAGGWNNLLGTRPHEYKARHGRSNSFNN
NEVHRSPPQQASHVGVPYPRLPQRVGQDVGDEPISGMISGKPPPIPGGGIPCKSSLAA
SIPTSBESRAPARAPAGATDGGQDNCPSAGQPCTDESGLRWRTYARWIHSGPVFWHFKPA
RPVNRASSYDSGYYAVRAHPPWIS"
a 13196 c 12804 g 19885 t 4295 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
join(<17378. 17578,17630. .17816,17864. .>18030)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
join(17378, 17578,17630, 17816,17864, 18030)
/gene="CG18160"
Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="FLYBASE:FBgn0039980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="CT40964"
/db_xref="FLYBASE:FBan0018160"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="FLYBASE:FBan0018160"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="CG18160 gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/protein_id="AAF45355.1"
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48.00

Quality:

alignment_scores:

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in Classes 1 to 1803.49

Birren, B., Fasman, K., McKernan, C., Nusbaum, C.,

Richardson, P., Lander, E., Baldwin, J., Barna, N., Beckerly, R.,

Richardson, P., Lander, E., Baldwin, J., Barna, N., Beckerly, R.,

Cantu, C., Castle, A., Chang, A., Cooke, P., Daly, M.J., Deppere, E.,

Cantu, C., Castle, R., Chang, B., Forrest, C., Gage, D., Gardyna, S.,

Gensheimer, S., Geralgery, K., Gilmartin, T., Gray, D., Hagos, B.,

Halphen, I., Hartis, K., Horton, L., Howland, J.C., Hung, J., Hul, L.,

Jacotot, L., Linton, L., MacKenzie, J., Marquis, N., McDermott, J.,

McEwan, P., McGurk, A., Medrim, J., Molla, M., Morris, W., Morrow, J.,

Nachman, A., Naylor, J., O'Connor, T., Olotu, A., Pavlin, B.,

Peterson, K., Roberts, D., Rollins, G., Roy, A., Sarnaik, A.,

Shyam, R., Stilwell, J., Stone, C., Strickland, C., Sydney, K., Tang, L.,

Vassiliev, H., Vo, A., Zemtseva, I., Zhao, J. and Zody, M.

Direct Submission 1997) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA
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S intren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Batren, B., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gago, D., Gardyna, S., Geraigery, K., Forrest, C., Funke, R., Gago, D., Gardyna, S., Geraigery, K., Grant, G., Macdonald, P., Marchan, P., McGurk, A., McKernan, K., Malort, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J., Mahfim, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J., Pavilin, B., Peterson, K., Rilbey, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Ye, W.J., Zhao, J. and Zody, M., Wheeler, J., Wu, Y., Wyman, D., Ye, W.J., Zhao, J., and Zody, M., Mheeler, J., Wu, Y., Wyman, D., Mille, M., Mander, A., Wheeler, J., Wingman, D., Ye, W.J., Zhao, J., and Zody, M., Astitute, M.T., Center for Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC003694 186314 bp DNA .ROD 01-SEP-1998
Mus musculus chromosome 19, clone CIT282B21, complete sequence.
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Location/Qualifiers
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Gaps: 0
Percent Identity: 69.231
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1 (bases 1 to 186314)
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                                   92.308
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08-881509-2 x AE003100/rev
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repeat_region complement(22047. 22237) repeat_region rept_family="B3" repeat_region complement(22302. 22398) repeat_region 7.pft_family="RSINE1" 22657. 22850 repeat_region rept_family="B2" repeat_region rept_family="B3" repeat_region remt_family="B3" remt_f		
/clone_lib="Research Genetics/Cal Tech CITB-HSP-C (plates 195-384)" /map="19" /chromosome="19" 507592 /rpt_family="Gc_rich" 515660 517660 517660 517660 518660 519660 519660 519660 519660 519660	Complement (1312) Complement (1312)	
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/db_xref="gdb=(513-60645.1"
/db_xref="G1:553669"
/translation="KGINGFEAEFKKSETSFHLTKPSAHMSDAAEYFCAVTFSGSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein, M.H., Concannon, P., Everett, M., Kim, L.D., Hunkapiller, T. and
                                                                                                                                                                                                                                                                                                                                                                                          Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                     C-region, J-region; T-cell receptor; V-region; antigen receptor; processed gene.
Human peripheral blood lymphocyte, cDNA to mRNA, clone AA27.
                                                                                                                                                                                                                                     HUMTCAZA 183 bp mRNA PRI 13-JAN-1995 HUMTCAZA HUMAT T-cell receptor active alpha-chain V-region (V-J-C) mRNA, partial cds, clone AA27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="T-cell receptor alpha-chain V-region (V-J-C)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diversity and structure of human T-cell receptor alpha-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variable region genes
Proc. Natl. Acad. Sci. U.S.A. 84 (19), 6884-6888 (1987)
88016194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 73.333
Percent Identity: 81.818
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                                                                                   Align seg 1/1 to: AC003694 from: 1 to: 186314
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                                                                                                                      1 TyrCysLeuValLeuSerGlySerAlaArgGln 11
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/map="14q11.2"
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Chromosome 14q11.2.
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M17666.1 GI:338805
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     Percent Similarity: 100.000
                                                                                                                                                                                           seq_name: gb_pr8:HUMTCAZA
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08-881509-2 x AC003694
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                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                  SOURCE
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This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X happing Group. Further information can be found at http://www.anger.ac.uk/HGP/ChrX 22212 is from the library RPC16 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pPAC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on Mar 24, 1999 this sequence version replaced gi:4469058.

On Mar 24, 1999 this sequence version replaced from overlapping clones.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

IMPORTANT: This sequence is not the entire insert of clone 22D12. IMPORTANT: This sequence is not the entire insert of clone 22D12. II may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/product="dA22D12.1 (novel protein similar to Drosophila
/product="dA22D12.1 (novel protein, KEL) and a heterogenous set of
other types of proteins)"
complement(1916..55943)
/gene="dA22D12.1"
/gene="dA22D12.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The true left end of clone 393P23 is at 69728 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MSTC repeat: matches 1. .405 of consensus" complement(join(1916. .3373,4913. .5084,34073. .34285, 35937. .36099,37414. .37638,44052. .44238,47425. .47637, 51717. .51913,55275. .55411,55801. .55943)
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                                                                                                                                                                                            LOCUS HS22D12 69827 bp DNA PRI 23-NOV-1999
DEFINITION Human DNA sequence from clone 22D12 on chromosome Xq21.1-21.33.
Contains a novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogenous set of other types of proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (18-MAR-1999) Sanger Centre, Hinxton, Cambridgeshire, Submitted 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 69827)
                                                                                                                                                                                    23-NOV-1999
102 TICTGTGTGTGTTTTTCTGGTTCTGCAAGGCAACTGACCTTT 146
                                                                                                                                                                                                                                                                                                                                                            Contains ESTs and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; KEL; Kelch; Ring Canal protein.
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/clone_lib="RPCI-6"
915._1335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                              seq_name: gb_pr6:HS22D12
                                                                                                                                                                            seg_documentation_block:
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/note-"match: proteins CE05435 CE18315 CE01951 CE00627 CE03539 072746 P32206 Q04652 CE14269 CE18133 Q14145 P28575 P21073 P24768 CE06293 073453; supported by GENSCAN and FGENES; start codon could also be on yet unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RWDPEGRQWNYVASMSTPRSTVGVYALNNKLYAIGGRDGSSCLKSMEYFDPHTNKWSL
CAPMSKRRGGVGVATYNGFLYVVGGHDAPASNHCSRLSDCVERYDPKGDSWSTVAPLS
VPRDAVAVCPLGDKLYVVGGYDGHTYLNTVESYDAQRNEWKEEVPVNIGRAGACVVVV
                                                                                                                                                                                                                                                                                                                                                                                         /translation="MNATRSEBQFHVINHAEQTLRKWENYIKEKQLCDVLLIAGHLRI
PAHRLVLSAVSDYFAAMFTNDVLEAKQEEVRMEGVDPNALNSLVQYAYTGVLQKEDT
IESLLAAACLLQLTQVIDVCSNFLIKQLHPSNCLGIRSFGDAQGCTELLNVAHKYTME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HFIEVIKNQEFLLLPANEISKLLCSDDINVPDEETIFHALMQWVGHDVQNRQGELGML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RDGLKTLNTVECFNPVGKIWTVMPPMSTHRHGLGVATLEGPMYAVGGHDGWSYLNTVE
                                                                                                                                                                                                                                            /evidence=not_experimental
/product="dA22D12.1 (novel protein similar to Drosophila
Kelch (Ring Canal protein, KEL) and a heterogenous set of
other types of proteins)"
/protein_id="CAB39994.1"
/db_xref="GI:4539520"
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3597. .36099,37414. .37638,44052. .44238,47425. .47637,
51717. .51913,55275. .55411,55801. .55943),
/gene="dAz2p12.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7348. 7558
/note="LIR37B repeat: matches 209. .411 of consensus" 7559. .7630
/note="LiMA4A repeat: matches 6222. .6296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7850. .9907 There are a 85% conserved. There are a 10015. .1045 repeat: matches 10. .1453 of consensus. 10431. .10738 repeat: matches 1. .308 of consensus. 10733. .11028 repeat: matches 1. .308 of consensus. 10733. .11028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7631. .7687
/note="LTR37B repeat: matches 411. .468 of consensus"
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//note="11P repeat: matches 4859. .4999 of consensus"

16657. 17002

//note="#HEIB repeat: matches 1. .364 of consensus"

17003. 18553

//note="#HEIB-INTERNAL repeat: matches 1. .1580 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7824. .8053
8/70te="MIR repeat: matches 4. .246 of consensus"
8/78. .2285
7.00te="Alusx repeat: matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5902. .7200
note="AluY repeat: matches 1. .298 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MIR_repeat: matches 85. .214 of consensus" 6902. .7200
                                                                                                                                                                                                upstream exon"
                                                                                                                                                                                                                          /codon_start=1
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18554. .18
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CDS
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/note="NERSA repeat: matches -943. .184 of consensus"
33335. .33506
/note="LiPBa repeat: matches -1544. .-1372 of consensus"
35655. .35727
/note="MERSA repeat: matches 10. .90 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="TIGGER2 repeat: matches 2131. .2185 of consensus"
                                                                                                                                                                                                                                                                                 20193. .21/34
/note="LiPBa repeat: matches -239. .1640 of consensus"
27763. .28810
/note="LiPBa repeat: matches -1537. .-420 of consensus"
28822. .31882
/note="LiPBa repeat: matches 184. ,4326 of consensus"
31883. .32181
                                                                                                     38170. 38307
/note="AluSg/x repeat: matches 134. .281 of consensus"
38382. 39020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39369. .39465
/notea LiPAA repeat: matches 6050. .6146 of consensus"
complement(39783. .40448)
/gene="dA22b12.1"
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40472. 40969
/note="match: GSS AQ17278"
41136. 41257
/note="LiPB2 repeat: matches 6030. .6152 of consensus"
/complement(41258. 41797)
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42731. 43039
7/note="LTR65 repeat: matches 315. .612 of consensus"
7/note="LTR64 repeat: matches 1. .660 of consensus"
7/note="MER4A repeat: matches 1. .660 of consensus"
L1 repeat: matches 3951. .4196 of consensus" .19450
                                              /note="L1 repeat: matches 4478. .4565 of consensus"
19451. .19738
/note="AluJo repeat: matches 1. .290 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38061. .38124
/note="MER4-internal repeat: matches 1110. .1171 of
                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSx_repeat: matches 1. .300 of consensus" 32182. .33314
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/note="30 copies 2 mer tt 73% conserved"
41975. .42030
/note="28 copies 2 mer aa 75% conserved"
complement(42597. .42781)
/gene="dA22D12.1"
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Gaps: 0
Percent Identity: 83.333
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/note="match: GSS AQ344849"
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91.667
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08-881509-2 x HS22D12/rev
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Ratio:
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J gene; junction; T cell receptor; TCR junctional sequence; V gene. human.
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(Dases 1 to 1318)
Jantzer, P.U. and Schendel, D.J.
Tymor-infilturating lymphocytes recognizing spontaneously arising renal cell carcinomas express T cell receptors characteristic of secondary immune response
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Submitted (11-JUN-1996) P. Jantzer, Institute for Immunology,
Goethestr. 31, D- 80336 Munich, FRG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS HSTCRJUNC 1318 bp mRNA PRI 08-JA DEFINITION H.sapiens mRNA for rearranged TCR junctional sequences.
ACCESSION X98410.
VERSION X98410.1 GI:1770560
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Schendel, D. J.
T-cells specific for kidney carcinoma
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TGCCTCGCTACTCGTTCTCCAAGGCAACTGACCTTT 36
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Sequence 7 from Patent EP0816496.
A93133
A93133.1 GI:6741522
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Jantzer, P.
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                      9b_pr8:S63879
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130184 ACOU769 DIOSOPPHIA melanoga

235457 AEO03708 DIOSOPHIA melanoga

117853 ACOU0703 DIOSOPHIA melanoga

117853 ACOU0703 Homo Sapiens PAC CI

140531 ACO46129 Homo Sapiens Chromo

158956 APO00791 Homo Sapiens Chromo

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20477 ACO05119 DIOSOPHIA melanogas

20484 UCO9513 Human Pigment Epithell

68379 ACO165119 DIOSOPHIA melanogas

115099 ACO1953 Human Pigment Epithell
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187 | AE003526 Drosophila melanoga
1 L42801 Homo sapiens (clone NS1-H
                                                                                      About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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i S63879 TCR V alpha -T cell r
i AF043886 Homo sapiens patient
i M17666 Human T-cell receptor
i U83242 Mus musculus D10 T-ce
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Patent: EP 0816496-A 07-JAN-1998;
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                                                                                                         /codon_start=1
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Schendel, D.J.
                                                             /rearranged
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365 c
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Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                         61.00
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LOCUS A93127
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BASE COUNT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 39)
                                                                                                                                                                                                                                                                     DEFINITION Human isolate M94 T-cell receptor alpha V-J junction (TCR Valpha ACCESSION 130448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dave, V.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L. Restricted usage of T-cell receptor V alpha sequence and variable-joining pairs after normal T-cell development and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (22-JUN-1995) Julia L. Hurwitz, St. Jude Children's Research Hospital, Immunology, 332 N. Lauderdale, Memphis, TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="T-cell receptor alpha V-J junction" /protein_id="AAA73621.1"
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Gaps: 0
Percent Identity: 69.231
Length: 13
Gaps: 0
Percent Identity: 84.615
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                                                                                                                                     Align seg 1/1 to: A93127 from: 1 to: 1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /isolate="M94"
/db_xref="taxon:9606"
/tissue_type="blood"
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Percent Similarity: 100.000
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Direct Submission
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                                          92.308
      57.00
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AC006244
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                               AUTHORS
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REFERENCE
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KEYWORDS
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Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 39)

                                                     HSU30428 39 bp mRNA PRI 01-AUG-1995
Human isolate M74 T-cell receptor alpha V-J junction (TCR Valpha
                                                                                                                                                                                                                                                        Dave, V.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L. Restricted usage of T-cell receptor V alpha sequence and variable joining pairs after normal T-cell development and bone
                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (22-JUN-1995) Julia L. Hurwitz, St. Jude Children's
Research Hospital, Immunology, 332 N. Lauderdale, Memphis, TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophija melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="T-cell receptor alpha V-J junction"
/protein_id="AAA73607.1"
/db_xref="GI:915482"
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/gene="TCR Valpha 3/J alpha 22"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="FCATSGSARQLIF"
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Hum. Immunol. 37 (3), 178-184 (1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="blood"
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AC018245.1 GI:6552946
HTG; HTGS_PHASE2.
                                                                                                                            U30428.1 GI:915481
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seg_name: gb_pr7:HSU30428
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                               seq_documentation_block:
                                                                                                                                                                                       Homo sapiens
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08-881509-3 x HSU30428
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Ratio:
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"E 2 (pases 1 to 92079)

S Celniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chave, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hostins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfelffer, B., Poon, L., Punch, E., Sequeira, A., Sethi, H., Snir, S., Zieran, L.L. and Rubin, G.M.

Zieran, L.L. and Rubin, G.M.

Direct Submission

L Submitted (22-DEC-1998) Drosophila Genome Center, Lawrence Berkeley, Laboratory, MS 64-121, Berkeley, CA 94720, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryotta; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Metazoa; Arthropoda; Tracheata; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 92079)

Celniker.S.E., Agbayani,A., Arcaina,T.T., Baxter.E., Blazej.R.G., Butenhoff.C., Champe,M., Chavez.C., Chew,M., Ciesiolkk.L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E., Ponk, S., Ponk, S., Syriskas,R.R., Man,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA HTG 30-JUL-1999 Drosophila melanogaster chromosome 2 clone DS00212 (D463) map 60F1-60F2 strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
                                                                                                                                                             This sequence was identified as CDM:10214018 by the submitter. For more information on this record e-mail to fly@celera.com.
* NOTE: This is a "vorking draft" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* Location/Qualifiers
                                                          Direct Submission
Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 83677
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Drosophila melanogaster"
/db_xref="taxon:7227"
22418 a 19303 c 19402 g 22554 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 12
Gaps: 0
Percent Identity: 83.333
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1 (bases 1 to 83677)
Adams, M. and Venter, J.C.
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HTG; HTGS_PHASE1.
fruit fly.
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LOCUS AC006244 92079 bp
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Percent Similarity: 83.333
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08-881509-3 x AC018245/rev
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Quality:
Ratio:
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  REFERENCE
                  AUTHORS
                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC007884 130344 bp DNA HTG 16-DEC-1999
Drosophila melanogaster chromosome 2 clone BACR08114 (D641) RPCI-98
08.1.14 map 60F-60F strain y; cn bw sp, *** SEQUENCING IN PROGRESS
***, 102 unordered pieces.
On Jul 28, 1999 this sequence version replaced gi:4836864.
For further information about this sequence, including its location and relationship to other sequence, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases. Pl library location:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Pl library, partial Sau3A in pNS582tet14Ad10"
/map="60P1-60P2"
20544 c 20168 g 25194 t 160 others
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Cachiker, S.E., Apbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Halkle, A., Hoskins, R.A., Huouston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M. Seew., Yu, C. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                           * arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                        * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                              525: contig of 525 bp in length 605: gap of unknown length 2501: contig of 1896 bp in length 2581: gap of unknown length 92079: contig of 89498 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: AC006244 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gabs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="y; cn bw sp"
/db_xref="taxon:7227"
/clone="DS00212 (D463)"
                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
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                                                                                                                                                                                                                                                                                  be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
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606
2502
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• Ratio:
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              COMMENT
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Numbricy Submission

Submitted (21-JUN-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA

Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Dec 16, 1999 this sequence version replaced gi:5670581.

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a "working draft' sequence. It currently consists of 102 contigs. The true order of the pleces are in out known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will

* be preserved.
2 (bases 1 to 130344)
Celniker.S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Dutenhoff,C., Champe,M., Chavec,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zleran,L.L. and
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gap of unknown length
contig of 1099 bp in length
gap of unknown length
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gap of unknown length
contig of 825 bp in length
gap of unknown length
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6060:
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1: contig of 100 bp in length
1: gap of unknown length
1: gap of unknown length
1: contig of 1094 bp in length
1: contig of 755 bp in length
1: contig of 857 bp in length
1: contig of 857 bp in length
1: gap of unknown length
1: gap of unknown length
1: contig of 810 bp in length
1: gap of unknown length
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g of 1073 bp in length
f unknown length
g of 1087 bp in length
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contig of 1264 bp in length
gap of unknown length
contig of 979 bp in length
gap of unknown length
contig of 1163 bp in length
gap of unknown length
                                                                                  g of 636 bp in length is unknown length of of 848 bp in length if unknown length of 1293 bp in length inknown length
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                                                                                                                                                                                                                                                                                                                        of 892 bp in length
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gap of unknown length
contig of 880 bp in length
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of 1210 bp in length
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Brachycera;
Pterryota; Metazoa; Endopterryota; Diptera; Brachycera;
Pterryota; Drosophilidae; Drosophila.

(CE 1 (bases 1 to 328500)

RS Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner M., Henderson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfelffer, B. Mah, K.C., Abril, J.F., Abayani, A., An, H.J., Beson, K.Y., Bernan, B.P., Blandari, D., Ballew, R.M., Beson, K.Y., Bernan, B.P., Bhandari, D., Bolshakov, S., Borkova, D., Botchan, M.R., Bouck, J., Brokstein, P., Brottier, P., Butlis, K.C., Busam, D.A., Butler, H., Cadleu, E., Center, A., Chandra, I.,
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LOCUS AE003465 328500 bp DNA INV 04-OCT-2000
DEFINITION Drosophila melanogaster genomic scaffold 142000013386038 section 14
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Ratio: 5.100
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08-881509-3 x AC007884
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                                                                                                                   /map="60D10-60D13"
                                                                                      /gene="CG13595"
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Cherry, J. M., Cawley, S., Dahlke, C., Davenport, L.B., Davies, P., de Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M., Dodson, K., Doup, L.B., Downes, M., Dugan Rocha, S., Dunkov, B.C., Dunn, P., Durbin, K.J., Evangelista, C.C., Ferraz, C., Ferriera, S., Fleischmann, W., Fosler, C., Gabrielian, A.E., Garg, N.S., Ferriera, S., Galbart, W.M., Glasser, K., Gladek, A., Gong, F., Gorrell, J.H., Gu, Z., Galbart, W.M., Harris, N.L., Harvey, D., Heiman, T.J., Hernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J., Kanison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Li, J., Li, Z., Liang, Y., Lin, X., Mattei, B., McIntosh, T.C., McIed, M.P., Moshrefi, A., Mount, S.M., Moy, M., Murphy, B., Murphy, L., Muszny, D.M., Nelson, D.L., Nelson, D.R., Nelson, K.A., Nixon, K., Muszny, D.M., Nelson, D.L., Nelson, D.R., Nelson, P.S., Parlby, J.M., Patleb, J.M., Patle, D., Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I., Stupski, M., Strong, R., Sunke, B., Striskas, R., Tector, C., Turner, R., Wenlst, C., Wu, D., Yang, S., Wang, Z.Y., Wassarman, D.A., Wenlst, C., Wu, D., Yang, S., Wang, Z.Y., Wassarman, D.A., Worley, K.C., Wu, D., Yang, S., Lao, W., Shue, R., Yeb, K.F., Shon, W., Shon, W., Shon, W., Shue, R., Yeb, Y., Yeb, R.F., Shon, W., Shon, W., Shon, W., Shon, W., Shue, B.C., Sheng, L., Zaveri, J.S., Zhan, M., Rhang, S. M., Worler, J.C., Zheng, X., Shon, W., Shue, R., Yeb, Y., Yeb, R., F., Zaveri, J.S., Zhan, M., Rhang, S. M., Wolley, Y., Suith, H.O., Gibbs, R.A., Myers, E. W., Rubin, G., Zhu, X., Smith, H.O., The genome sequence 287 (5461), 2185-2195 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIVSSAGSLAGSKLGRFIDTHDIVMRFNHAPTQGHEVDVGSKTTIRVVNSQVVTKPEF
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SVWRLWQSLQMFAGNRPISKNPPSSGFIGLALLLPHCPQVDFVEYVPSTRLNGRCHYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 328500)
Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
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Location/Qualifiers
1. .328500
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SGDCAVVPAATTRCTIPYYAGGGAVAKPPTQLLVWLSALLGLLSSCGAARQRWSCOW
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repeat_region
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                 TITLE
JOURNAL
                                                                                                                    FEATURES
                                                                                  COMMENT
AC005\overline{3}50 78661 bp DNA PRI 31-JUL-1998 Homo sapiens chromosome 5, BAC clone 261j17 (LBNL H190), complete
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 78661)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Kadnerly,W., Miguel,T., Miller,C., Pitluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
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Join (52695. ,53722,54265. .>54357)

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AC005350
AC005350.1 GI:3366562
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Ricke, D.O.
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AUTHORS
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Direct Submission
Submitted (31-JUL-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94-20, U.S.A.
Sequence submitted by:
DOE Joint Genome Institute.
                                                                                                                                                                                                                                               476. 656
/rpt_family="Alu"
2704. 2839
/note="GRAIL 2 excellent exon, frame 0"
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/note="GRAIL 2 excellent exon, frame 0" 31846. 31869
/note="(TA)12"
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/rpt_unit=AC
complement(39057. .39133)
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39883. .40023
                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(10780. .14299)
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complement(15044. .15135)
/rpt_family="MIR"
complement(16072. .16399)
/rpt_family="LINE"
19038. .19075
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complement(29199, .29244)
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/db_xref="taxon:9606"
/map="5q"
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complement(34387..3
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complement(19076.
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25177, .27648
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24716. .24995
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/rpt_unit=T
                                                                                                                                                                                                 /clone="261j17"
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/note="(T)21"
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/note="GRAIL 2 excellent exon, frame 1"
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Percent Identity: 69.231
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a 14357 c 14140 g 24597 t
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complement(74279. 75083)
/rpt_family="L1"
75262. 75289
/note="(AC)14"
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conplement(57418. .57744)
/rpt_family="Alu"
57577. .5750
                                                                                                                                                                                                                                                                                                                                                                            complement(63432, .63490)
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complement(65010, .66136)
/rpt_family="L1"
                                                                                                                    complement(45953. .46019)
/rpt_family="MIR2"
46124. .46204
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complement (72044. .72130)
/rpt_family="L1"
complement(40416. .40487)
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complement(66461. .66710)
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77696. .77815
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Consensus quality: 185996 bases at least Q40
Consensus quality: 197156 bases at least Q30
Consensus quality: 197156 bases at least Q30
Consensus quality: 199406 bases at least Q20
Estimated insert size: 194000; agarose-fp estimation
Estimated insert size: 204969; sum-of-contigs estimation
Quality coverage: 8.77 in Q20 bases; agarose-fp estimation
Quality coverage: 8.10 in Q20 bases; unm-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
consists of 30 contigs. The true order of the pieces

* is not known and their order in this sequence record is
runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 207869)

DOE Joint Genome Institute.
                                               29-JUN-2000
                                              AC073697 207869 bp DNA HTG 29-JUN-20 Mus musculus clone RP23-161111, WORKING DRAFT SEQUENCE, 30
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1715: gap of unknown length
3162: contig of 1347 bp in length
3162: contig of 1327 bp in length
4489: contig of 1327 bp in length
4589: gap of unknown length
678: contig of 2174 bp in length
6863: gap of unknown length
7948: contig of 1085 bp in length
8048: gap of unknown length
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2 (bases 1 to 207869)
DOE Joint Genome Institute.
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seq_name: gb_htg17:AC073697
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                                   seq_documentation_block:
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111844
117307
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148028
151124
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170586
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                  REFERENCE
AUTHORS
                                             TITLE
JOURNAL
       JOURNAL
                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 231260)
DOE Joint Genome Institute.
Sequencing of Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AC073735 231260 bp DNA HTG 18-JUL-2000
DEFINITION MUS musculus clone RP23-25C2, WORKING DRAFT SEQUENCE, 24 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI mouse BAC library 23"
48520 c 48115 g 55879 t 2907 others
                                                                                                                                                                                                                                                                                                                                                                 126692: gap of unknown length
139568: contig of 13476 bp in length
139668: gap of unknown length
155125: contig of 15457 bp in length
155225: gap of unknown length
207869: contig of 52644 bp in length.
                                                                                                                                                                                                                                            10267 bp in length
                                                                                                                                                                                                                                                                                                                 gap of unknown length contig of 7715 bp in length gap of unknown length contig of 10027 bp in length
               length
bp in length
                                                                                                                                                                          gap of unknown length contig of 6039 bp in length gap of unknown length contig of 7909 bp in length
                                                     bp in length
                                                                                bp in length
                                                                                                                                  contig of 6871 bp in length
gap of unknown length
contig of 4763 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                      gap of unknown length
contig of 5336 bp in length
gap of unknown length
                                                                                                          bp in length
                                                                                                                                                                                                                                                                         contig of 6194 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: AC073697 from: 1 to: 207869
                                           ength
                                                                      ength
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                                                                                                                          length
                                                                                                                                                                                                                                  unknown length
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                                                                                                                                                                                                                                                              unknown length
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contig of 3330 b
gap of unknown 1
gap of unknown 1
contig of 4082 b
contig of 4082 b
gap of unknown 1
contig of 4467 b
gap of unknown 1
contig of 8783 b
gap of unknown 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-161111"
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AC073735.2 GI:9256774
HTG: HTGS_PHASE2; HTGS_DRAFT.
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                                                                                                                                                                                                                                gap of
contig
gap of
                                     42439:
                                                      46521:
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08-881509-3 x AC073697/rev
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42340
42440
                                                                46522
46622
51089
51189
59972
60072
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71806
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78045
85954
86054
96321
96421
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139569
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155126
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
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ORIGIN
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
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Consensus quality: 217735 bases at least 040
Consensus quality: 226530 bases at least 040
Consensus quality: 226530 bases at least 030
Consensus quality: 227843 bases at least 030
Consensus quality: 227843 bases at least 030
Estimated insert size: 239600; agarose-fp estimation
Estimated insert size: 239600; agarose-fp estimation
Cuality coverage: 7.12 in 020 bases; agarose-fp estimation
Quality coverage: 7.39 in 020 bases; sum-of-contigs estimation.

* NOTE: This is a working draft' sequence. It currently
consists of 24 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
                                                Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94599, USA
On Jul 18, 2000 this sequence version replaced gi:8810352.
-----Genome Center
Center: Joint Genome Institute
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 18749 8848: gap of unknown length

* 8849 36011: contig of 27163 bp in length

* 36012 36011: gap of unknown length

* 36112 44018: gap of unknown length

* 44019 48586: contig of 7807 bp in length

* 44019 48586: contig of 16266 bp in length

* 48587 48686: gap of unknown length

* 48587 64952: contig of 16266 bp in length

* 64953 70887: contig of 5835 bp in length

* 70988 107221: contig of 36234 bp in length

* 70988 107221: contig of 36234 bp in length

* 70988 107221: contig of 36234 bp in length

* 70988 107221: contig of 36234 bp in length
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contig of 8001 bp in length
gap of unknown length
gap of unknown length
contig of 11598 bp in length
gap of unknown length
gap of unknown length
contig of 3096 bp in length
gap of unknown length
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of 11598 bp in length
unknown length
of 3096 bp in length
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unknown length
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unknown length
of 1675 bp in length
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Center clone name: RPCI-23_25C2
2 (bases 1 to 231260)
DOE Joint Genome Institute.
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gap of
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ORIGIN

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ELVVPPKPIQNAFDSISYFRDAWLRKLSHKGQVLKSSIADVVACYSSEKRKLYQKAAD
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                                                                                                                                                 2424. .3440
/standard_name="ORF3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TyrCysLeuAlaThrGlySerAlaArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fruit fly.
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC014160.1 GI:6437175
HTG; HTGS_PHASE2.
                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34220 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rockville, MD, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 5.333
Percent Similarity: 100.000
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08-881509-3 x SCWFUSPRO/rev
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LOCUS AC014160
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                                                                                                                                                                                                                                                                                                                                                                        1065
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ORIGIN
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SOURCE
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protein_laAaA47456.1"
/db_xref="G1:310360"
/translation="MKSKRVVGLPAVSAGLKVCVHQTSLHNMIVSLERRVFRVKNAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEGINFDARMWAVDAFMLLMPFYTEOMERVVDDFCSFTQESKI.EDCLELDPSVNEFPD
EEVKKRDEEGVMVLQRTSSRKHIKRVRAGMMQAAIKAVEKRIINRHTIFGDDMGKVDE
AAVRATASDICGEFKINEHHTNVLVYAAAYLAMTPDQRSIDSVKLAYNPKSQARRTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MGFISFSLFDVDKLLVWVSKFNPGKILSSICNLGVDCWNRFRKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotic sequence of Sweet clover necrotic mosaic dianthovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sweet clover necrotic mosalc virus unidentified genes, three complete cds's including fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sweet clover necrotic mosaic virus"/strain="59"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; SSENA positive-strand viruses, no DNA stage;
Tombusviridae; Dianthovirus.
I (bases 1 to 3876)
Ge,Z., Hiruki,C. and Roy,K.L.
   200238: contig of 13533 bp in length 200338: gap of unknown length 206497: contig of 6159 bp in length 20855: gap of unknown length 208755: contig of 2158 bp in length 208855: gap of unknown length 231260: contig of 22405 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sweet clover necrotic mosaic virus (strain 59) RNA. Sweet clover necrotic mosaic virus
                                                                                                                                                                                                                              /clone_lib="RPCI mouse BAC library 23"
52031 c 52510 g 62847 t 2307 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /standard_name="fusion protein"
121. .831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 231260
                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/protein_id="AAA47455.1"
/db_xref="GI:310359"
                                                                                                                                                                          /organism="Mus musculus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:28348"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                            /clone="RP23-25C2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3876 bp ss-RNA
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4.042
92.308
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LOCUS SCWFUSPRO
                                                                                                                                                                                                                                                                                                                                                                                                                                   08-881509-3 x AC073735
                                                               206498
206598
208756
208856
                            200239
200339
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                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
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TFYRECFPGDOLEOLIKWOLTNTGSALLPFGELVRYRTKVCRMSGDINTGLGOKTLM
CSMVHAFLKETGVRASLANNGDDCVLFCEKGDYEGINRULEOWFLCRSFEMTYBKPVD
VLEKVVPCRSOPVCLATQWANRQLGESLSRDCFSTQDMLNPRTFKDANNALGCOKGTI
NDGVPFHMAQAKLMHKSAETGSSTRRELHKOMEYRRRRRRAFKTRANNALWSEVEDATRLS
YFRAFSIEPYVQRIVEEYLSOVEVTCEGRETNVLPTHYSRLHKDLIKSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPTKAALHTQIVLSVVGSIALHANNGKASQRFRLNPSNPALFPTIAYFAANYDMYRMK
KLTLRYVPLYTVQNSGRVAMIWDPDSQDSVPQSRQETSAVSRSISTAAYTEKGSLTIPA
DOWGRRVADSSNVDRKLVDYGQLLFVNHSGSEGIETGDYFLECEVEFKGPQPTATVVO
RGIIDDRGVLTGEGFSYLLPTDYTTATGISMNLDVAGTYLVTLYVTSSGSGRNQVLG
NSTLVGDFRTAYSGINFIATFGISMNLDVAGTYLVTLYTSYGSGSGNLOVLG
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*** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAA47457.1"
/db_xref="GI:310361"
/translation="MSTKAPKKSKQRSKPRNRNPSTSVKTVTIPFAKTQIVKTVNPPP
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DAIDDVFGEKTVLSGLDNRAQGRAIAHKWRKYQNPIGIGLDASRFDQHCSVDALKFEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

(bases 1 to 34220)
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/db_xref="taxon:7227"
1 8026 c 7649 q 9103 t
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2950: contig of 1410 bp in length
29530: contig of 1410 bp in length
30654: contig of 1624 bp in length
30734: gap of unknown length
32691: contig of 1024 bp in length
32771: gap of unknown length
32771: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: contig of 932 bin length
1: gap of unknown length
1: contig of 1167 bp in length
1: gap of unknown length
1: contig of 1648 bp in length
1: gap of unknown length
1: contig of 1832 bp in length
1: contig of 830 bp in length
1: gap of unknown length
                                                                                                                                                                                                                                                contig of 1000 bp in length gap of unknown length contig of 117 bp in length contig of 589 bp in length gap of unknown length contig of 804 bp in length contig of 804 bp in length gap of unknown length
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contig of 1079 bp in length
contig of 805 bp in length
gap of unknown length
gap of unknown length
contig of 860 bp in length
gap of unknown length
contig of 983 bp in length
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                                                                                      of 547 bp in length
unknown length
                                                                                                                                                   682 bp in length
                                                                                                                                                                                                       of 608 bp in length
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gap of unknown length
contig of 1364 bp in length
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contig of 1383 bp in length
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of 1035 bp in length
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of 1245 bp in length
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gap of unknown length
contig of 1227 bp in length
gap of unknown length
contig of 954 bp in length
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of 1386 bp in length
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of 2258 bp in length
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of 1344 bp in length
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                                                                  unknown length
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DO MAT 2, 2000 this sequence version replaced 91:697945.
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence to bdgp@fruitfly.berkeley.edu All contigs in this submission meet the following cutoffs: length >= 200 bases.
* NOTE: This is a "working draft sequence record is consists of 86 contigs. The true order of the pieces is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as "This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS
AC007648 130184 bp DNA
DEFINITION Drosophila melanogaster chromosome 3 clone BACR13A02 (D705) RPCI-98
13.A.2 map 88E-88F strain y; cn bw sp, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pierygota; Nacoptera; Intellegate Discophila and Poetrygota; Deperation of Partygota; Deperation of Partygota; Diptera; Brachycera; I (basea I to 130184)

Celniker,S.E., Apbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L., Hinkle,A., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Wolley,P., Yang,S., Sethi,H., Svirskas,R., Wan,K.H., Webster,D., Woolley,P., Yang,S., Ree,M., Yu.C. and Rubin,G.M. Webster,D., Sequenching of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Kan, R.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Sylfskas, R.R., Wan, K.H., Weinburg, T., Zehni, H., Snir, E., and
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9: gap of unknown length
8: contig of 969 bp in length
8: gap of unknown length
6: contig of 1068 bp in length
6: gap of unknown length
7: contig of 748 bp in length
4: contig of man length
                                                                                                                                                      Align seg 1/1 to reverse of: AC014160 from: 1 to: 34220
Percent Similarity: 91.667 Percent Identity: 75.000
                                                                                                                                                                                                                                             6686 TTTTGCTTGGCTGGGCTCGGCAGCAACA 6651
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                                                                        alignment_block:
08-881509-3 x AC014160/rev
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length

Page 12

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is gap of unknown length of gap of unknown length is contig of 3380 bp in length is contig of 3382 bp in length is gap of unknown length is gap of unknown length is contig of 5181 bp in length is contig of 5835 bp in length is gap of unknown length is contig of 5879 bp in length is contig of 756 bp in length is gap of unknown length is gap of unknown length is contig of 756 bp in length is contig of 633 bp in length
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contrig of 2182 bp in length
contrig of 1812 bp in length
contrig of 1813 bp in length
gap of unknown length
contrig of 1943 bp in length
contrig of 1881 bp in length
contrig of 1881 bp in length
gap of unknown length
gap of unknown length
contrig of 3863 bp in length
contrig of 2430 bp in length
contrig of 2430 bp in length
contrig of 2430 bp in length
gap of unknown length
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                                                             contig of 1164 bp in length gap of unknown length contig of 2015 bp in length gap of unknown length contig of 1832 bp in length
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contig of 501 bp in length
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12

Length: Gaps:

alignment_scores:
Quality: 47.00
Ratio: 4.273

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AC004897 Homo sapiens PAC
1 AC004695 Homo sapiens BAC
1 AC034147 Homo sapiens chr
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CLVVLGGSQGNLIFGXCLVGFNNAGNMLTFGXXCLVARNGRNCSDLW"
329 c 344 t 87 others
                                                                                                                                                                                                                                                                                          gene.
                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Butheria; Primates; Catarthini; Hominidae; Homo.
1 (bases 1 to 1318)
Jantzer, P. U. and Schendel, D. J.
Tymor-infiltrating lymphocytes recognizing spontaneously arising renal call carcinomas express T cell receptors characteristic of secondary immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION Human isolate M94 T-cell receptor alpha V-J junction (TCR Valpha ACCESSION U30448
                                                                                                                                                                                                                                                                                 J gene; junction; T cell receptor; TCR junctional sequence; V human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (11-JUN-1996) P. Jantzer, Institute for Immunology,
Goethestr. 31, D- 80336 Munich, FRG
Location/Qualifiers
                                                                                                                                                                                              08-JAN-1997
                                                                                                                                                                   seq_documentation_block:

LOCUS HSTCRJUNC 1318 bp mRNA
DEFINITION H.sappiens mRNA for rearranged TCR junctional sequences.

ACCESSION X98410
       22484
90731
149572
163015
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Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
2 (bases 1 to 1318)
Jantzer,P.
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Ratio: 5.167
Percent Similarity: 100.000
                                                                                                                       seq_name: gb_pr7:HSTCRJUNC
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AUTHORS
TITLE
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AUTHORS
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JOURNAL
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1.6e+03
1.9e+03
2.0e+03
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2002.78
1190.47
1191.02
1145.55
1140.48
1140.27
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1139.95
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102.
163.
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OM of: 08-881509-5 to: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search information block:
Query: 08-881509-5
Query length: 13
Database: GenEmbl:*
Database sequences: 1118133
Database length: -1736092196
Search time (sec): 3669.890000
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                                                                                                                                                            Command line parameters:
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gb_om:AF111089
gb_om:AF111088
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gb_btg RAC020380
gb_htg RAC020380
gb_htg RAC020380
gb_htg RAC020380
gb_htg RAC03289
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9b_pr7:HSTCRJUNC

9b_pr7:HSU30448

9b_pat1:A93127

9b_pr7:HSU30428

9b_pat1:A93133

9b_omi.A93133

9b_omi.OAPGES

9b_omi.OAPGES
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BASE COUNT
ORIGIN
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 39)
Dave, W.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L. Restricted usage of T-cell receptor V alpha sequence and wariable-joining pairs after normal T-cell development and bone marrow transplantation. Hum. Immunol. 37 (3), 178-184 (1993)
                                                                                                                                                                                                                                                                                             Submitted (22-JUN-1995) Julia L. Hurwitz, St. Jude Children's Research Hospital, Immunology, 332 N. Lauderdale, Memphis, TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="r.cell receptor alpha V-J junction"
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11 c 8 9 15 t
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Percent Identity: 76.923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="TCR Valpha 3/J alpha 22"
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Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
Location/Qualifiers
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1. .54
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                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="blood"
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                                                                                                                                                                                                                                                                                                                                                                                                           /isolate="M94"
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Schendel, D.J.
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U30448.1 GI:915515
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Percent Similarity: 100.000
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                                                     Homo sapiens
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Ratio:
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                                                                                                         REFERENCE
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             KEYWORDS
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SSCDVKLVEKSFETDTNLNFQNLSVIGFRILLLKVAGFNLLMTLRLMSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 39)
1 (bases 1 to 39)
2 back, V.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L.
Restricted usage of T-cell receptor V alpha sequence and variable-joining pairs after normal T-cell development and bone marrow transplantation
Hum. Immunol. 37 (3), 178-184 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION Human isolate M74 T-cell receptor alpha V-J junction (TCR Valpha 3/J alpha 22) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-JUN-1995) Julia L. Hurwitz, St. Jude Children's Research Hospital, Immunology, 332 N. Lauderdale, Memphis, TN 38101, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="T-cell receptor alpha V-J junction"
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Gaps: 0
Percent Identity: 84.615
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    .804
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Ratio:
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BASE COUNT 3
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and Fishman, M.C.
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AUTHORS
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                                TITLE
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211968 Zebrafish AB Danio rerio STS genomic, sequence tagged site.
G39068
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
1 (bases 1 to 604)
                                                         Percent Identity: 76.923
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Percent Identity: 83.333
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                                                                                                                                                                      1 TyrCysLeuAspSerGlySerAlaArgGlnLeuThrPhe 13
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Schendel,D.J.
T-cells specific for kidney carcinoma Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
LOCALION/Qualifiers
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Sequence 7 from Patent EP0816496.
A93133
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91.667
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                      Quality: 53.00
Ratio: 4.818
Percent Similarity: 84.615
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LOCUS A93133
                                                                                                                                                                                                                                                                                                                                                                      unidentified.
unidentified
                                                                                                                                                                                                                                                                                                                                                                                                         unclassified
                                                                                                                                                                                                                                         seq_name: gb_pat1:A93133
                                                                                   alignment_block:
08-881509-5 x HSU30428
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08-881509-5 x A93133
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Ratio:
Percent Similarity:
        alignment_scores:
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/dev_stage="Adult"
/lab_host="DH5alphaF'IQ"
/lab_host="DH5alphaF'IQ"
/note="Vector: ml3MP19 with added BatXI site; V-type:
Phage: Genomic DNA from a single adult zebrafish of AB
strain was digested with Alui, Cac8!, HaeIII, NIaVI, or
Rsal. Fragments in the range of 250-500 bp were gel
purified and a BatXI linker was added. The fragments were
cloned into a modified M13mp19 vector and transformed
into E. Coli DH5alpha. Microsatellilite sequences were
screened with labeled d(CA)15 and d(GT)15 oligonucleotide
                                                                                                                     Contact: Mark C. Fishman
Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 6177265806
Shimoda, N., Knapik, E.W., Ziniti, J., Sim, C., Yamada, E., Kaplan, S.
                                            A genetic linkage map of the zebrafish with 2000 microsatellite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primers are available from Research Genetics Inc.
                                                                                                                                                                                                                                                                                                                                                                                           Presoak: 94 degrees C for 5.0 minutes
Denaturation: 94 degrees C for 1.0 minute
Annealing: 58 degrees C for 1.0 minute
POlymerization: 72 degrees C for 1.5 minute
PCR Cycles: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 13
Gaps: 0
Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (http://www.resgen.com phone: 800-533-4363)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.5 mM
50 mM
10 mM
8.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermal Cycler: MJ Research PTC-100
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                                                                                                                                                                                                                                                  Email: fishman@mgh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
Primer A: TCTGGAGGACACAGTGTGF
Primer B: TGCACAGTAACCACTCAGC
STS size: 147
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 ng
each 375 nM
each 200 uM
: 0.034 units/ul
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/clone_lib="Zebrafish AB"
/sex="F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. 604
/organism="Danio rerio"
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160 g
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Tris-HCl:
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237. .256
complement(364. .
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                                                                                          Unpublished (1998)
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/product="mature prostaglandin endoperoxide synthase (AA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGIPPOSOMAVGOEVEGLIPGIMIYATIWLREHNRVCDLLKARHPTWGDEQLFOTARL
ILIGETIK VIEEVVQQLSGYFLQLKFDPELLFGAOFOYRNIAMERVALYHHPLMP
DISERVGADYSYEQFLFNTSMLVDYGVBALVDAFSRQPAGRIGGGRNIDHTLHVAVD
VIKERVLRLOPFNEYRRFGARFYTSFQELTGEKERNASLELETGYGDLDALEFYPGLL
LEKCHPNSIFGESMIEMGAPFSLKGLLGNPICSPEYWKASTFGGEVGFNLVKTATLKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VNATFITRDTLARLVITVRSNI.IPSPPTYNIAHDYISWESFSNVSYYTRILPSVPRDCP
TPMDTKGKKQLPDAEFLSRRFLLRRKFIPDPQSTNLMFAFFAQHFTHQFFKTSGKMGP
GFTKALGHGVDLGHIYGDNLERQYQLRLFKDGKLKYQMLNGEVYPPSVEEAPVLMHYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SWISS PROT:P05979"
/translation="MSRQSISLRFPLLLLLLSPSPVFSADPGAPAPVNPCCYYPCQHQ
GICVRFGLDRYQCDCTRTGYSGPNCTIPEIWTWLRTTLRPSPSFIHFLLTHGRWLWDF
                                                                                                                                                                                                                                                                                                                                                                             Tanabe T.

Subrect Submission

Submitted (05-APR-1988) Tanabe T., National Cardiovascular Center
Research Institute, 5-7-1 Fujishiro-dai, Suita, Osaka 565, Japan

Z. (Dasses I to 2011)

Yokoyama, C., Takai, T. and Tanabe, T.

Primary structure of sheep prostaglandin endoperoxide synthase
PEBS Lett. 231 (2), 347-351 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="prostaglandin endoperoxide synthase precursor (AA
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae;
                                                                                                                                               23-MAR-1995
                                                                                                                                                                  Sheep mRNA for prostaglandin endoperoxide synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="pot. N-linked glycosylation site" 2595. .2600 /note="pot. polyA signal" 2611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nnote="pot. N-linked glycosylation site" 49. .351
                                                                                                                                                                                                                              prostaglandin endoperoxide synthase; synthase.
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                        1 TyrCysLeuAspSerGlySerAlaArgGlnLeuThrPhe 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="vesicular gland"
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/db_xref="G1:1362"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Ovis aries"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9940
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                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="polyA site"
743 c 707 g
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                                                                                                                                               2611 bp
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                                                                                                                           seq_documentation_block:
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                                                                                   seq_name: gb_om:OAPGES
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40. .111
112. .1839
112-duct="mature peptide of prostaglandin endo
peroxidase"
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40. .1844
/product='prostaglandin endo peroxidase of
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae;
                                                                                                                                                                                                                                                                               29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA CODING PROSTAGLANDIN ENDOPEROXIDE SYNTHETASE PATENT: JP 1989228479-A 1 12-SEP-1989; MEIJI MILK PROD CO LTD
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                                                                                                                                                                                                                                                                               CDNA encoding prostaglandin endo peroxidase.
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                                 Percent Identity: 75.000
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Key Location/Qualifiers
                                                                                                                                                                             2150 TGCCTAAATTCCGGATCAACTAGAAATCTGACATTC 2115
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 Length:
                                                                                                                        Align seg 1/1 to reverse of: OAPGES from: 1
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/organism="Ovis aries"
/db_xref="taxon:9940"
a 746 c 705 g (
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strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sheep,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP 1989228479-A/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          topology: Linear;
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anti-sense: No;
                                                                                                                                                                                                                                                                                                                                 E02077.1 GI:2170319
JP 1989228479-A/1.
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mat_peptide
Quality: 48.00
Ratio: 4.000
Percent Similarity: 100.000
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08-881509-5 x E02077/rev
                                                                        alignment_block:
08-881509-5 x OAPGES/rev
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LOCUS
                                                                                                                                                                                                                             seq_name: gb_pat1:E02077
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Bos taurus Percent Similarity: 99148828 1390 Ratio: alignment_scores: ACCESSION VERSION KEYWORDS SOURCE ORGANISM BASE COUNT REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS JOURNAL CDS FEATURES TITLE TITLE ORIGIN DSFRYGPODYSYEQFLENTSHLVDYGVEALVDAFSROPAGRIGGGRRIDHHILHVAVD VIKESRVLRLOPFNEYRKRFGMKPYTSFQELTGEKEMAAELEELYGDIDALEFYPGLL LEKCHPNSIFGESMIEMGAPFSLKGLLGNPICSPEYWKASTFGGEVGFNLVKTATLKK /protein_id="AaA31576.1" /db_xref="G1:166036" /translation="MSRQSISLRFPLLLLLLSPSPVFSADPGAPAPVNPCCYYPCQHQ TPMGTKGKKOLPDAEFLSRRFILLRRFIPDPQGTNLMFAFFAQHFTHQFFKTSGKMGP GFTRALGKOVDLGHIYGDNLBRQYQFLRFKDGKHYQMLNGBYYPPSVBEAPVLMHYP RGIPPQSQMAVGQFYGLLFGLMLTATIRENHNVODLLKAEHPWGDEQLFGTARL ILIGETIKIVIEEYVQQLSGYFLQLKFDPELLFGAQFQYRNRIAMEFNOLYHMHPLMP GICVRFGLDRYQCDCTRTAIPAPTAPSRRYGPGSGRLCGPAPLSSTFMLTHGRWLWDF VNATFIRDTLMRLVLTVRSNLIPSPPTYNIAHDYISWESFSNVSYYTRILPSVPRDCP Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Draft entry and computer-readable sequence for [1] kindly provided seq_documentation_block: LOCUS AF111086 4912 bp mRNA MAM 04-MAR-1999 DEFINITION Bos taurus latrophilin 3 splice variant abag mRNA, complete cds. Bovidae: Caprinae; Octs. 1 (base: Caprinae; Ovis. 2 (base: Caprinae; Ovis. DeWitt.D.L. and Smitt.W.L. Primary structure of prostaglandin G/H synthase from sheep vesicular gland determined from the complementary DNA sequence Proc. Natl. Acad. Sci. U.S.A. 85, 1412-1416 (1988) 27-APR-1993 prostaglandin G/H synthase signal peptide" /note="prostaglandin G/H synthase precursor (EC SHPPGS 2666 bp mRNA MAM 2°. Sheep prostaglandin G/H synthase mRNA, complete cds J03599 prostaglandin synthase. Sheep vesicular gland, cDNA to mRNA, clone PGHS-ov. /note="prostaglandin G/H synthase mRNA" LVCLNTKTCPYVSFHVPDPRQEDRPGVERPPTEL" 165. .1892 Gaps: 0 Percent Identity: 75.000 /note="prostaglandin G/H synthase" 760 c 737 g 628 t 2150 TGCCTAAATTCCGGATCAACTAGAAATCTGACATTC 2115 2205 TGCCTAAATTCCGGATCAACTAGAAATCTGACATTC 2170 Length: 2 CysLeuAspSerGlySerAlaArgGlnLeuThrPhe 13 Align seg 1/1 to reverse of: SHPPGS from: 1 /organism="Ovis sp." /db_xref="taxon:9939" by D.L.Dewitt, 19-JAN-1988. Location/Qualifiers /codon_start=1 1.14.99.1)" J03599:1 GI:166035 . 2666 .1895 .164 Ratio: 4.000 Percent Similarity: 100.000 1. .2666 /note=' alignment_block: 08-881509-5 x SHPPGS/rev seq_documentation_block: seq_name: gb_om:AF111086 Unreported. seq_name: gb_om:SHPPGS Quality: Ratio: Ovis sp. alignment_scores: sig_peptide mat_peptide source DEFINITION ORGANISM JOURNAL MEDLINE COMMENT BASE COUNT REFERENCE AUTHORS mRNA ACCESSION VERSION KEYWORDS SOURCE FEATURES TITLE ORIGIN

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FAVLMAHVEVKHSDAVHDLLLDVITWVGILLSLVCLLICIFTFCFFRGLQSDRNTIHK
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FESEHSRRKYFYLVGYGMPALIVAVSAAVDYRSYGTDKVCWLRLDTYFIWSFIGPATL
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                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-DEC-1998) Biochemistry Department, Imperial College, Exhibition Road, London SW7 2AY, UK
Location/Qualifiers
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Matsushita, H., Lelianova,V.G. and Ushkaryov,Y.A.
He latrophilin family: multiply spliced G protein-coupled receptors with differential tissue distribution
FEBS Lett. 443 (3), 348-352 (1999)
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Matsushita, H., Lellanova, V.G. and Ushkaryov, Y.A.
Direct Submission
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1153 c 1091 g 1278 t
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/organism="Bos taurus"
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164. .3859
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FKTRQCQMAKQPCPAGTIGVSTYLCLAAPGIWDPQGPDLSNCSSPWVNHITQKLKSGE
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OKRERSCRAYVQAWYETVNILLQPQALNAMRDLTTSDOLRAATWLLDTVEESAFVLAD
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PVVFTVKHIKQSEENFNPNCSFWSYSKRTMTGYWSTQGCRLLTTNKTHTTCSCNHLTN
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TWAFGLMYINESTVIMAYLFTIFNSLQGMFIFIFFCVLQKKVRKEYGKCLRTHCCSGR
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DPLQASDKIYYMPWTPYRTDTLTEYSSKDDFIAGRPTTTYKLPHRVDGTGFVVYDGAL
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NLCISLFVAELLFLIGINRTDQPIACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEV
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Bos taurus latrophilin 3 splice variant abbg mRNA, complete cds.
                                                                                                                                                                                                                                                        Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A.
The latrophilin family: multiply spliced G protein-coupled
receptors with differential tissue distribution
FEBS Lett. 443 (3), 348-352 (1999)
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NKLVNNLGSGSEDDAIVLDDATSFNHEESLGLELIHEESDAPLLPPRVYSTENHQLHH
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PPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSSDGFIVPPNKDGTPPEGSSK
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                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A.
Direct Submission
Submitted (04-DEC-1998) Biochemistry Department, Imperial College,
Exhibition Road, London SW7 2AY, UK
AF111085 4989 bp mRNA MAM 04-MAR-1999
Bos taurus latrophilin 3 splice variant abaf mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 4989)
Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A.
The Latrophilin family: multiply spliced G protein-coupled receptors with differential tissue distribution
FEBS Lett. 443 (3), 348-352 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=experimental
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Gaps: 0
Percent Identity: 69.231
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                                                                                                    AF111085.1 GI:4164052
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                                                                                                                                                                               COW.
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Bos

ORGANISM

AUTHORS TITLE

REFERENCE

DEFINITION

sed_name:

ACCESSION VERSION

KEYWORDS

SOURCE

source

CDS

EATURES

TITLE JOURNAL

MEDLINE REFERENCE

JOURNAL

AUTHORS

5016

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DPLQASDKIXXMPWTPYRTDTLTEYSSKDDFIAGRPTTTYKLPHRVDGTGFVVYDGAL
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NLLKTDTVREWTDNIQDLEVARLSTEGNLEDLKFPRWTGHGSTIQLGANTLKQNGRNGE
IRVACYVRHIKGSYERNENSMKLGTEGNAETHSVIVNSPVITAAINKEFSNKYYLAD
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IIMLNVIFLGIALYKWFHHTAILKPESGCLDNIKSWVIGAIALDFFTTAGFFFT
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TROUNGKI TU 15GCLNPYTRIEGTWODTAYDKREASANEMIGCILTYVKKSYEDDDDNEA
TGNKIDY I YNTDOSKOSLVDPPFPNSYOY TAAVDY NEPDNLLYVWNYHVYKYSLDFG
PLDSRSGQAHHGQVSY I SPPIHLDSDLERPPVREI STTGPLGTGSTTTFTTLETTWO
FGRSTTPSVGRRNRSTSPEALEVLANDITTHVPSARQPITALESCEAVERREIM
FRIRGGOMAKQPPCAGT I GYGSTYLCLAPDGTNDPOCEDISNCSSPWNNHITOKLKSGE
TAANIARELAEGTRNHLNAGDITYSVRAMDQLVGLLDVOLRNLTPGGKDSSARSLNKI
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KTSGSRTPGRYSTGSOSRIRRMWNDTVRKOSESSFITGDINSSASLNRCAMANHLISN
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (pases 1 to 5041)
Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A.
Direct Submission
Submitted (04-DEC-1998) Biochemistry Department, Imperial College,
                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS AF111087 5041 bp mRNA MAM 04-NAR-1999
DDETUITION Bos taurus latrophilin 3 splice variant abah mRNA, complete cds.
ACCESSION AF111087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 5041)
Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A.
The latrophilin family: multiply spliced G protein-coupled
receptors with differential tissue distribution
FEBS Lett. 443 (3), 348-352 (1999)
                                                                                                                                                                                                                                                      2077 CATTGCCTGGACATAGGCTCTGCAAGAGCGCTCTTTT 2039
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                                                                                                                           Align seg 1/1 to reverse of: AF111088 from: 1
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164. .3988
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Location/Qualifiers
1. 5041
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                                                     08-881509-5 x AF111088/rev
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            alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence-experimental
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STENHQLHHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDSLYTSMPALAGVPTAES
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Mammalla, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A. Direct Submission Submitted (04-DEC-1998) Biochemistry Department, Imperial College,
                                                                                                                                                                                                 AF111088 5016 bp mRNA MAM 04-MAR-1999
Bos taurus latrophilin 3 splice variant abbf mRNA, complete cds.
AF111088
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Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A.
He latrophilin family: multiply spliced G protein-coupled receptors with differential tissue distribution
FEBS Lett. 443 (3), 348-352 (1999)
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Percent Identity: 69.231
2077 CATTGCCTGGACATAGGCTCTGCAAGAGCGCTCTTTT 2039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exhibition Road, London SW7 2AY, UK Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                 AF111088.1 GI:4164058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 5016)
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4.364
84.615
                                                                                                                                                                                seq_documentation_block:
LOCUS
                                                                                                          gb_om:AF111088
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Ratio:
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13

alignment_scores:

BASE COUNT

ORIGIN

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ATEQNICATIVE SQLIPSTILE GTWDTAYDKRSASNAFWICGILIVVKSVYEDDDNEA TGRKIDY I VATDQSKDSLVDVFFPRSYQIAAVDYRFRDNILIVWNYHVVKSLDEG TGRKIDY I VATDQSKDSLVDVPFPRSYQY I AANDYRFRDDILLIVWNYHYVKYSLDFG PGRKIDY I VATDQSKQQAHIGQVQY I SPPILLDSDLERPPVREISTTGFGTTTTTTWS PGRSTTPSVSGRRRASTSTE BEAT IEVLUDITHVPSASPQIPALESCESVERAEIWWFKTRQQQMAKQPCPAGTIGVSTYLCLAADGIWDDQGPDLSNCSSPWVNHITQKLKSGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OKRERSCRAYVQAMVETVNNLLOPQALNAWRDLTTSDQLRAATMLLDTVEESAFVLAD
NLLKTDIYPRRYTDNIQLEVARLSTEGRENEDLKFPBYRGHGSTQLSANTLKRONSRNGE
IRVAFVLYNNLGPYLSTERASMKLGTERAMSTHRSVINSPVITAALINKEFSNRYYLAD
PVYFTYKHIKOSEBRIPRNGSFWSYSKRYMHOYWSTQGCRLLTTNKTHTTCSCNHLTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAVLMAHVEVÄHSDAVHDLLLDVITWVGILLSLVCLLICIFTFCFFRGLQSDRNTTHK
NLCISLFVAELLFLIGINRTDQPIACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IIMLNVIFLGIALYKMFHHTAILKPESGCLDNINYEDNRPFIKSWVIGAIALLCLLGL
STARFCLMYTNRSTVINAYTFITRNSLOGMFIFFHCYLDKYKRKRKGKCLFHTCKSGR
STAESIGGGKTSGSPPGKYSTGSORIRRWNDTVRKGSESSFITGDINSSASLING
AMANHIISNALLRPHGTNNPYNTLLGEPAVCNNPSVSMYNAQEPYRETSMGVKLNIAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MWPSQLLVFMMLLAPIIHAFSRAPIPMAVVRRELSCESYPIELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPGTDVIMIESANYGRIDDKICDSDPAQMENIRCYLPDAYKIMSGRCNNRTQCAVVAG
PDVPPDPCPGTYKYLEVQYECVPYKVEQKVFLCPGLLKGVYQSEHLFESDHQSGAWCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPLQASDKIYYMPWTPYRTDTLTEYSSKDDFIAGRPTTTYKLPHRVDGTGFVVYDGAL
FFNKERTRNIVKFDLRTRIKSGEAIIANANYHDTSPYRWGGKSDIDLAVDENGLWVIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAANIARELAEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (04-DEC-1998) Biochemistry Department, Imperial College,
Exhibition Road, London SW7 2AY, UK
                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LoCUS AFT11090 5068 bp mRNA MAM 04-MAR-1999
DEFINITION BOS taurus latrophilin 3 splice variant abbh mRNA, complete cds.
ACCESSION AF111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A. Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A. The latrophilin family: multiply spliced G protein-coupled receptors with differential tissue distribution FEBS Lett. 443 (3), 348-352 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="latrophilin" 3 splice variant abbh"
/protein_id="AAD05326.1"
/db_xref="GI:4164063"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 5068)
Matsushita,H., Lelianova,V.G. and Ushkaryov,Y.A.
                                                                                                                                                   Align seg 1/1 to reverse of: AF111087 from: 1 to: 5041
Percent Identity: 69.231
                                                                                                                                                                                                                                              2077 CATTGCCTGGACATAGGCTCTGCAAGAGCGCTCTCTTT 2039
                                                                                                                                                                                                                 1 TyrCysLeuAspSerGlySerAlaArgGlnLeuThrPhe 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF111090.1 GI:4164062
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Percent Similarity: 84.615
                                                          alignment_block: 08-881509-5 x AF111087/rev
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KEYWORDS
SOURCE
ORGANISM
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JOURNAL
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AUTHORS
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REFERENCE
AUTHORS
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alignment_scores:

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AP001980 Homo sapiens
AL356112 Homo sapiens
AC027539 Homo sapiens
AC018429 Homo sapiens
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J gene; junction; T cell receptor; TCR junctional sequence; V gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor-infiltrating lymphocytes recognizing spontaneously arising renal cell carcinomas express T cell receptors characteristic of secondary immune response
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutherla;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1318)
Jantzer, P. U. and Schendel, D. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (11-JUN-1996) P. Jantzer, Institute for Immunology,
Goethestr. 31, D- 80336 Munich, FRG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JAN-2000
                                                                                                                                                                                                               HSTCRJUNC 1318 bp mRNA PRI 08-JA
H.sapiens mRNA for rearranged TCR junctional sequences.
X98410
              152641
155124
167960
169801
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CysLeuValValSerGlySerAlaArgGlnLeuThrPhe 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .1318
/organism="Homo sapiens"
/isolate="batients 22 and 26"
/db.xref="taxon:9606"
              3.8e+03
3.9e+03
4.2e+03
4.2e+03
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A93131
              95.19
95.07
94.47
94.39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
2 (bases 1 to 1318)
Jantzer,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A93131.1 GI:6741520
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45.00
45.00
45.00
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Percent Similarity: 100.000
                                                                                                                                                     seq_name: gb_pr7:HSTCRJUNC
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                                                                                                                                                                                                      seq_documentation_block:
LOCUS HSTCRJUNC
DEFINITION H.sapiens mRN
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Ratio:
           gb_htg23:AP001980
gb_htg21:AL356112
gb_htg13:AC027539
gb_htg6:AC018429
                                                                                                                                                                                                                                                                                                                                                                          human.
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ACCESSION
VERSION
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VERSION
KEYWORDS
SOURCE
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AUTHORS
TITLE
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1318 | x98410 H.sapiens mRNA for rear 39 | A93131 Sequence 5 from Patent EF 42 | AJ235208 Homo sapiens mRNA for T 1341 | A93127 Sequence 1 from Patent B7 | L42801 Homo sapiens (clone NSI-F 214 | 140776 Human T-cell receptor al 716 | S63879 TCR V alpha =T cell receptor al 716 | S63879 TCR V alpha =T cell recept 1758 | AE003100 Drosophila melanogas 51 | AF04388 Homo sapiens patient CS 917580 | AC05515 Homo sapiens chromod 183137 | AC016140 Homo sapiens chromod 18719 | AC016319 Homo sapiens chromod 18719 | AC06925 Homo sapiens chromod 18719 | AC016319 Homo sapiens chromod 1870 | AC01238 Homo sapiens chromod 1870 | AC012488 Homo sapiens chromod 1870 | AC01248 Homo sapiens chromod 1870 | AC01248 Homo sapiens chromod 1870 | AC01248 Homo sapiens patient CS 1 AF04387 Homo sapiens patient CS 1 AF04387 Homo sapiens patient CS 1 AF04388 Homo sapiens chromod 12021 | AE00866 Human isolate MJ01 T-cell 65 | X02886 Human isolate MJ01 T-cell 65 | X02886 Human isolate MJ01 T-cell 65 | X02886 Human solate MJ01 T-cell 7467 | X64414 M Musculus mRNA for low 12021 | AE008073 Hallobacterium sp. NR 12021 | AC021752 Homo sapiens chromod 123751 | AC021752 Homo sapiens chromod 123751 | AC021752 Homo sapiens chromod 123761 | AC021752 Homo sapien
                                                                                                                                                                                                            About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
        out_format : pfs
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1.2e+03
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126.50
328.71
1.8e+03
2.5e+03
3.1e+03
3.4e+03
3.6e+03
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0.0013
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1.53
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OM of: 08-881509-6 to: GenEmbl:*
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Query length: 14
Database: GenEmbl:*
Database sequences: 1118133
Database length: -1736092196
Search time (sec): 3669.890000
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9b_pri: HUMYCRACG

9b_pri: HUMYCRACG

9b_pri: HUMYCRACG

9b_pri: AF004388

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gb_pr8:HUMTCRADCV
gb_htg8:AC021752
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gb_htg9:AC022407
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Jb_pr6:HSA235208
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Sequence
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FEATURES

ORIGIN

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seq_documentation_block:
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-OCT-1998) Cross S.M., Queensland Institute of Medical Research, The Bancroft Centre, 300 Herston Road, Brisbane, AUSTRALIA 4029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Crossreactive recognition of viral, self, and bacterial peptide ligands by human class I-restricted cytotoxic T lymphocyte clonotypes: implications for molecular mimicry in autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T cell receptor; T cell receptor alpha chain; variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 42)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 42)
Misko,I.S., Cross,S.M., Khanna,R., Elliott,S.L., Schmidt,C.,
Pye,S.J. and Silins,S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 96 (5), 2279-2284 (1999)
99162595
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/cell_type="cytotoxic T lymphocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 4.692 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 92.308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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/haplotype="A1, A2, B8, B45, Bw6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CysLeuValValSerGlySerAlaArgGlnLeuThrPhe 14
                                                                                               T-cells specific for kidney carcinoma
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
                                                                                                                                                                                                                                                                                                              /translation="CLVLSGSARQLTF"
                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
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    .39
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                                                                                                                                                       Location/Qualifiers
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AJ235208.1 GI:3851223
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                                                                 1 (bases 1 to 39)
Schendel, D.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                   61.00
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                unidentified.
                                  unidentified
unclassified
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AUTHORS
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KEYWORDS
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VERSION

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ATNDY ITWYQOFPSGGPRFIIOGYKTRYTNEVASLETPADRKSSTLSLERVSLSDTAV
YYCLVGGSARQLTFGGSGTQLTVLDDIQNPDPAVYQLRDSKSSDKSVCLFTDFDSGTNV
SQSKDSDVY ITDKTVLDMRSMDFKSNSAVAWSNKSDFACANAFNNS II PEDTFFPSPE
SSCDVKLVEKSFETDTNLNFQNLSVIGFRILLLKVAGFNLLMTLRLWSS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JAN-2000
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Gaps: 0
Percent Identity: 84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 TACTGCCTC...GTGGGTGGTTCTGCAAGGCAACTGACCTTT 348
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                                                                                                                                                                                                                                                                                                                 2 CysLeuValValSerGlySerAlaArgGlnLeuThrPhe 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 1341)
Schendel, D. J.
T-cells specific for kidney carcinoma
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
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                                    16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unidentified"
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1. .804
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                                        φ
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1..42
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84.615
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LOCUS A93127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unidentified
unclassified
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Clonal expansion of myelin basic protein-reactive T cells in patients with multiple sclerosis: restricted T cell receptor V gene rearrangements and CDR3 sequence
                                                                                                                                                                                                                                                      Vandevyver, C., Mertens, N., van den Elsen, P., Medaer, R., Raus, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 214)

Kurnick, J.T., Ihara, P., Pervaiz, S., Pandolfi, F., Van, Den Elsen P., Waltkus, R., Boyle, L.A., Hishii, M. and Andrews, D.M.

T-cell receptor usage by anti-melanoma specific cytotoxic tumor-infiltrating lymphocytes. Detection of dominant tumor-specific T-cell clones by single strand conformational polymorphism and T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSU40776 214 bp mRNA PRI 07-DEC-1995
Human T-cell receptor alpha chain (TCRAV2S1J22) mRNA, partial cds.
                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 87)
HUWTCRACG 87 bp mRNA PRI 07-NOV-1995
Homo sapiens (clone NSI-:F4) T cell receptor alpha chain (TCRA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Partial TCRVA (1. .15), TCRNA (16. .18), TCRJA (19. .75), partial TCRCA (76. .87)" /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"T cell receptor alpha chain"
/protein_id-"AAA80064.1"
/db_xref-"G1:853663"
/translation-"YFCASGSRQLTFGSGTQLTVLPDIQK"
19 2 1 9 27 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 71.429
                                                                                        L42801.1 GI:853662
T cell receptor alpha.
Homo sapiens (clone: NSI-F4) cDNA to mRNA.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 TTTGGGAGGCCTCTGGTTCTGCAAGGCAACTGACCTTT 45
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                                                                                                                                                                                                                                                                                                                                                                              Immunol. 25 (4), 958-968 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NS1-F4"
/map="14911.2"
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="TCRA"
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                                                mRNA, partial cds.
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LOCUS HSU40776
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Ratio:
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                                                                    ACCESSION
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KEYWORDS
                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 716)
Griesinger, F., Jansen, B. and Kersey, J.H.
Differentiation in mature T lymphoid leukemia cells is unstable and reversible to myeloid cells, without the involvement of a common
                   2 (bases I to 214)
Kurnick, J.T., Ihara, A., Pervalz, S., Pandolfi, F., Van, Den Elsen P.,
Waitkus, K., Boyle, L.A., Hishii, M. and Andrews, D.M.
Direct Submission
Submitted (16-NOV-1995) James T. Kurnick, Pathology Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCR V alpha =T cell receptor variable alpha chain (human, MT-ALL, Genomic Mutant, 716 nt).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genbank staff at the National Library of Medicine created this entry (NCBI gibbsq 63879] from the original journal article. This sequence comes from Figure 4.
                                                                                                                              Laboratory, Massachusetts General Hospital, 149 East 13 St.,
Charlestown, MA 02129, USA
                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MU 57"
1. .214
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1. .716
                                                                                                                                                                   Location/Qualifiers
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/note="TCR V&agr"
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9
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09
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08-881509-6 x HSU40776
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seq_documentation_block:
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Bukaryota; Metazoa; Arthropda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 66222)

Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,

Adams, M.D., Celniker, S.E., Richardas, S., Ashburner, M., Henderson, S.N.,

Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, O., Chen, L.X.,

Brandon, R.C., Rogers, Y.H., Blazel, R.G., Champe, M., Pfeiffer, B.D.,

Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor

Miklos, G.L., Abril, J.F., Agbayani, A., An, H.J.,

Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A.,

Baxendale, J., Bayraktaroglui, Ballew, R.M., Basu, A.,

Benos, P.V., Berman, B.P., Blandari, D., Bottier, P., Burtis, K.C.,

Busam, D.A., Butler, H., Cadieu, E., Center, A., Chandra, I.,

Cherry, J.M., Cawley, S., Dahlke, C., Davenport, L.B., Davies, P., de

Pablos, B., Deltcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M.,

Dodson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dunkov, B.C.,

Dunn, P., Durbin, K.J., Evangelista, C.C., Ferrazo, C., Ferriera, S.,

Kennison, Y.A., Harris, M.L., Harvey, D., Heiman, T.J.,

Kennison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C.,

Kravitz, S., Kulp, D., Lang, Y., Liu, X., Mattel, B., McIntosh, T.C.,

Li, J., Li, Z., Liang, Y., Lia, X., Mount, S.M., Muzny, B., Murphy, L.,

Muzny, D.M., Nesherfi, A., Mount, S.M., Moy, M., Murphy, B., Murphy, L.,

Muzny, D.M., Nusskern, D.R., Nalson, D.R., Nusn, K.,

Nusskern, D.R., Parleb, J.M., Palazzolo, M., Pittman, G.S., Pan, S.,

Pathanola, W., Paneleb, J.M., Palazzolo, M., Pittman, G.S., Pan, S.,

Pathanola, W., Paneleb, J.M., Palazzolo, M., Pittman, G.S., Pan, S.,

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YSGTYPGGSSTOLITYLEVLEVLTASQLS
189 c 177 g 183 t
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Drosophila melanogaster genomic scaffold 142000013385418, complete
join(58 ..109,340. .>716)
/gene="TCR V alpha"
/note="This sequence comes from Figure 4; conceptual
translation presented here differs from translation in
publication"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 0
Percent Identity: 71.429
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92.857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                          197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
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SOURCE
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                                          CDS
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Pollard, J., Puri, V., Reese, M.G., Reinert, K., Remington, K., Saunders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I., Simpson, M., Skupski, M.P., Smith, T., Spier, E., Spradling, A.C., Stapleton, M., Strong, R., Sun, E., Svirskas, R., Tector, C., Turner, R., Venter, E., Wang, A.H., Wang, X., Wang, Z.Y., Wassarman, D.A., Weinstock, G.M., Weissenbach, J., Williams, S.M., Woodage, T., Worley, K.C., Wu, D., Yang, S., Yao, Q.A., Ye, J., Yeh, R.F., Zaveri, J.S., Zhan, M., Zhang, G., Zheng, L., Zheng, K.H., Shong, F.N., Zhong, W., Zhou, S., Zhu, S., Zhu, X., Smith, H.O., Gibbs, R.A., Myers, E.W., Rubling, G.M. and Venter, J.C.

Sience 287 (5461), 2185-2195 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEVHRSPPQQASHVGVPYPRLPQRVGQQVGQEPISGMISQKPPPIPGQGIPCKSSLAA
SIPTSPSESAAPASATDSGQPNCPSAAGQFCTDESGLRWRTYARWIHSGPVFWHFKPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF043888 51 bp mRNA PRI 11-NOV-1998
Homo sapiens patient CS-1 clone AV228 T cell receptor alpha chain
STOR3 (TCRA) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                              20196006
20196006
2.0 (bases Leo 68222)
Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
Direct Submission
Submitted (21.MAR-2000) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .17578,17630. .17816,17864. .>18030)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
join(17378. .17578,17630. .17816,17864. .18030)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18042 a 13196 c 12804 g 19885 t 4295 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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Percent Identity: 76.923
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<17378 .>18030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="FLYBASE:FBgn0039980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="CG18160 gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: AE003100 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(<17378..1
/gene="CG18160"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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alignment_scores:
                                                                                                                                                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                    gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular basis of cross-reactivity among allergen-specific human T cells: T-cell receptor V alpha gene usage and epitope structure Immunology 81 (1), 15-20 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS S69140 98 bp mRNA rat berning and a second second forman, DEFINITION TCR V alpha-T-cell receptor alpha-chain (allergen-specific) [human, grass-sensitive individual VI 19, peripheral blood, mRNA Partial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Contains the 3' end of the TCRAV/TCRBV, the nDn/n, and the 5' end of the TCRAJ/TCRBJ." /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 98) Mohapatra, S.S., Mohapatra, S.S.,
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="from rheumatoid arthritis patient CS-1 [TCRAV1S3]
                                                                                                                                                                                                                                                                                                                                           C (bases 1 to 51)

Striebich, C.C., Falta, M.T., Wang, Y., Bill, J. and Kotzin, B.L.

Birect Submission
Submitted (21-JAN-1998) Pediatrics, National Jewish Medical and Research Center, 1400 Jackson St., Denver, CO 80206, USA
                                                                                                             1 (bases 1 to 51)
Striebtch, C.C., Falta, M.T., Wang, Y., Bill, J. and Kotzin, B.L. Selective accumulation of related CD4+ T cell clones in the synovial fluid of patients with rheumatoid arthritis J. Immunol. 161 (8), 4428-4436 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human peripheral blood grass-sensitive individual VI 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="T_cell receptor alpha chain CDR3"
/protein_id="AAC72683.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 73.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="synovial fluid"
/clone="AV228"
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    .51
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [TCRAJ22]"
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86.667
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LOCUS
                                         Homo sapiens
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ORGANISM
                                 ORGANISM
                                                                                                                                                                         AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                        MEDLINE
REFERENCE
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JOURNAL
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VERSION
KEYWORDS
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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

"I (basea 1 to 17758)

"R Muzny,D.M., Adams,C., Bailey,M., Barbaria,J., Blankenburg,K.,
Bodota,B., Bouck,J., Bowle,S., Brooks,A., Buhay,C., Bunac,C.,
Burkett,C., Burrows,J., Carter,M., Chack,J., Cort., Cox.C.,
David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N.,
Dugan-Rocha,S., Durbin,K.J., Fernandez,C., Ferraguto,D.,
Porcum-Transey,J., Frantz,P., Ganesh,R., Gorrell,L.L.,
Guevara,W., Harris,K., Hernandez,C., Ferraguto,D.,
Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y.,
Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y.,
Lichtarge,O., Liu,J., Liu,W., Logan,O., Lozado,R.J., Lu,J.,
Lucier,R., Martin,R., Martinez,C., McLeod,M.P., Mei,G., Morgan,M.,
Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,R., Nguyen,R.,
Shah,E., Shan,H., Simon,M., Samuel,S., Say,J., Scherer,S.,
Tabor,P., Taylor,T., Vasquez,L., Vinson,R., Volo,, Wahbah,M.,
Matlington,S., Weinstock,G., Weinstock,I.R., Williamson,A., and
                                                                                                                                                                                                                                                                                                                                                                           /partial
/gene="TCR V alpha"
/note="This sequence comes from Fig. 3b; Protein sequence
is in conflict with the conceptual translation"
GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 144562] from the original journal article. This sequence comes from Fig. 3a.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /exception="Protein longer than coding region shown; mismatch(12[E->G])"
/product="T-cell receptor alpha-chain"
/protein_id==N00144.1"
/db_xref="G1:545974"
/translation="DSATYFCAALPESAROLIFGSGTQLTVLPDIQN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens chromosome 3 clone RP11-20F9, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces.
AC069515
                                                                                                                                                                                                                                                                                   /gene="TcR V alpha"
/note="T-cell receptor alpha-chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 14
Gaps: 0
Percent Identity: 64.286
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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HTG; HTGS_PHASE1.
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LOCUS AC069515 177580 bp
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08-881509-6 x S69140
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REFERENCE AUTHORS TITLE JOURNAL

COMMENT

TITLE JOURNAL

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4027 others
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37561 c 36782 g 50297 t
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gap of unknown 1
contig of 1890 b
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gap of unknown 1
contig of 1474 b
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                                                 contig of 3578 b
gap of unknown l
contig of 3360 b
gap of unknown l
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/db_xref="taxon:9606"
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                    Submitted (02-UUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 5, 2000 this sequence version replaced gi:8705299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17112: contig of 17112 bp in length
17212: gap of unknown length
29649: contig of 12437 bp in length
29749: gap of unknown length
39046: contig of 9297 bp in length
39146: gap of unknown length
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Contact: hgsc-help@bcm.tmc.edu
                                                                                                                              Center: Baylor College of Medicine
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Direct Submission
Unpublished
2 (bases 1 to 177580)
Worley, K.C.
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123347:
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HOMO sapiens chromosome 2 clone RP11-480F1, WORKING DRAFT SEQUENCE, ACCOUNTING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                          Direct Submission
Submitted (09-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 183137) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 10 conties. The true order of the pleces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                         Jul 7, 2000 this sequence version replaced g1:8568870.
                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center
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5619: gap of unknown length
2937: contig of 7318 bp in length
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                                                                                  HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                               AC017084.5 GI:8954420
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Waterston, R.H.
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                                                  AC017084
              DEFINITION
                                                                                                                     ORGANISM
                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
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REFERENCE
AUTHORS
                                                ACCESSION
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KEYWORDS
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/organism="Homo sapiens"

Location/Qualifiers

source

FEATURES

/db_xref-"taxon:9606'

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Homo sapiens chromosome 3 clone RP11-568N1, WORKING DRAFT SEQUENCE, 18 unordered pieces.
                                                                                                                                                                                                                                                                                                                                       904 others
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 83.333
                                                                                                                                                                                                     48126. .59707 / note="assembly_name:Contig13" 59808. .74780 / note="assembly_name:Contig14"
                                                                                                                                                                                                                                                                                 ture 90144. 122272"

/note="assembly_name:Contig16"

ture 122373. 183137

/note="assembly_name:Contig17"

51158 a 39133 c 38659 g 53283 t
                                                                                                  13038. .23638 //note="assembly_name:Contig10" 23739. .34806
                                                                                                                                                                              34907. .48025
/note="assembly_name:Cont1g12"
48126. .59707
                                                                                                                                                                                                                                                                      /note="assembly_name:Contig15"
                                                                         5620. 12937
/note="assembly_name:Contig9"
                                                                                                                                        /note="assembly_name:Contig11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .5519
/note="assembly_name:Contig8
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          /clone="RP11-480F1"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                               vector_side:right"
                                                                                                                                                                  vector_side:left"
/chromosome="2"
                                                                                                                                                        clone_end:SP6
                                                                                                                                                                                                                                                           .90043
                                                  clone_end:T7
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91.667
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LOCUS AC069255 18
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08-881509-6 x AC017084
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                                                                                                    misc_feature
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TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

COMMENT

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                                                                                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: Estimated insert size may differ from sequence length

* NOTE: This is a "working draft' sequence. It currently

* NOTE: This is a "working draft' sequence. It currently

* consists of 18 contigs. The true order of the pieces

* is not known and thair order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                        Direct Submission
Submitted (23-MAY-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Aug 13, 2000 this sequence version replaced gi:9690226.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-terminator Big. Dye: 89% of reads chemistry: Dye-terminator Big. Dye: 89% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 168848 bases at least 040 Consensus quality: 176853 bases at least 030 Consensus quality: 176853 bases at least 020 Estimated insert size: 180247; sum-of-contigs estimation Quality coverage: 0x in 020 bases; agarose-fp estimation Quality coverage: 4x in 020 bases; sum-of-contigs estimation
Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, O., Wahbah, M., Watlington, S., Weinstock, G., Weinstock, I.R., Williamson, A., Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42030: contig of 42030 bp in length
42130: gap of unknown length
73896: contig of 31766 bp in length
73996: gap of unknown length
92026: contig of 18030 bp in length
92126: gap of unknown length
107548: contig of 15422 bp in length
107648: gap of unknown length
124195: contig of 16747 bp in length
134255: gap of unknown length
137477: contig of 13182 bp in length
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of 9741 bp in length
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Center code: BCM
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----- Summary Statistics
Sequencing vector: M13; L08821
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                                                                                                                    (bases 1 to 187419)
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124295:
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107648:
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                                                                            Direct Submission
Unpublished
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107549
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183304
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 86524)

Muzny, D. M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,

Bodota, B., Bouck, J., Brooks, A., Buhay, C., Bunac, C.,

Burket, C., Burrows, J., Carter, M., Chen, Z., Cox, C.,

David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,

Dugan-Roccha, S., Durbin, K. J., Fernandez, C., Ferraguto, D.,

Forcum-Tansey, J., Frantaz, P., Ganesh, R., Gorrell, J. H., Gorrell, J. J., Jackson, L. L. Jackson, R. Nayen, R. Samuel, S. Say, J. Scherer, S. Shah, E. Shen, H. Simon, M. Samuel, S. Say, J. Scherer, S. Shah, E. Shen, H. Simon, M. Samuel, S. Say, J. Scherer, S. Tabor, P. Tapor, P. Tapor, P. Tapor, P. Vasquez, L. Vinson, R. Vo, Q. Wahbah, M. Shah, E. Shen, H. Simon, M. Samuel, S. Nayen, R. Nay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens chromosome 10 clone RP11-110, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.
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On Sep 5, 2000 this sequence version replaced gi:8655885.
                                                                                                                                                                                                                                                                                                                                                                                                                              1749 others
184776: contig of 1373 bp in length
184876: gap of unknown length
186142: contig of 1266 bp in length
186242: gap of unknown length
187419: contig of 1177 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: AC069255 from: 1 to: 187419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 12
Gaps: 0
Percent Identity: 83.333
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Center: Baylor College of Medicine
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                                                                                                                                                                                        Location/Qualifiers
1. 187419
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                         /clone="RP11-568N1"
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AC016140.10 GI:9966744
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LOCUS AC016140 86524 bp
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Unpublished
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08-881509-6 x AC069255/rev
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186143
186243
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Chemistry: Dye-terminators Big 1008 of reads Sequencing vector: M13: L08821
Chemistry: Dye-terminator Big Dye: 1008 of reads Assembly program: Phrap; version 0.990329
Consensus quality: 73224 bases at least Q40
Consensus quality: 78615 bases at least Q30
Consensus quality: 78615 bases at least Q30
Consensus quality: 78615 bases at least Q30
Consensus quality: 81740 bases at least Q30
Consensus quality: 81740 bases at least Q30
Estimated insert size: 7631; agarose-fp estimation
Quality coverage: 2.4x in Q20 bases; agarose-fp estimation
Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 8 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary, Gammen the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17560: contig of 17560 bp in length 17660: gap of unknown length 37182: contig of 19422 bp in length 37182: gap of unknown length 53268: contig of 16086 bp in length 63134: contig of 12766 bp in length 66234: gap of unknown length 72391: contig of 6725 bp in length 72391: gap of unknown length 73391: gap of unknown length 73391: gap of unknown length 73391: contig of 6720 bp in length 73391: contig of 6720 bp in length
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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26011 a 17662 c 16032 g 26107 t
                                                     Center project Information
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                                                                                                                 Center clone name: RP11-110
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ORIGIN
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alignment_scores:

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences. Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < le-34) to the EST and CDNA sequences. Genes demonstrate at least two exons

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

ANNOTATION OF FEATURES:

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(CE 1 (bases 1 to 172581)

RS Muzny, D.M., Adams, C., Balley, M., Barbaria, J., Blankenburg, K., Bodota, E., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C., Burrows, J., Carter, M., Charko, J., Chen, Z., Cox, C., David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N., Dugan-Rocha, S., Durbin, K. J., Fernandez, C., Ferraguto, D., Gorrell, L.L., Guevara, W., Harris, K., He, X., Hernandez, J., Hodgson, A., Hogues, M., Harris, K., He, X., Hernandez, J., Hodgson, A., Hogues, M., Harris, K., He, X., Hernandez, J., Hodgson, A., Hogues, M., Harris, K., He, X., Hernandez, J., Lackson, L., Jia, Y., Jones, M., Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Lu, M., Logan, O., Lozado, R. J., Lu, J., Lucier, R., Martin, R., Martinez, C., Macheod, M. P., Melson, A., Nguyen, R., Morris, R., Martin, R., Martinez, C., Mash, S., Nelson, R., You, Borrer, S., Shah, E., Shen, H., Samuel, S., Say, J., Scherer, S., Shah, E., Shen, H., Vasquez, L., Vinson, R., Vo, O., Wabbah, M., Wallington, S., Weinstock, G., Weinstock, I. R., Williamson, A., Wolley, K., Wren, J., Wensision

AL Unpublished

Se Gorrell to 172581)
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Worley, K.C.

Direct Submission

Submitted (25-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (Baylor Plaza, Housto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (16-AGC-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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                                                AC009319.19 GI:9558561
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Worley, K.C.
Direct Submission
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Direct Submission
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flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

FEATURES

338. .6929 / /note="Unigene cluster similar to: SEG_HSLPP Human lipoma /rpt_family="(CA)n" 15652. 15996 /note="Region similar to: Hs#S1813459 ul-HF-NBO-alf-f-08-0-UI.rl Homo sapiens CDNA: AW503943" complement(16516. 17018) /note="Region Similar to: Hs#S1739629 UI-H-BWO-ajp-d-04-0-UI.sl Homo sapiens cDNA: AW298030" 17132. .17835 /note="Region similar to: Hs*S2010443 EST387857 Homo sapiens cDNA: AW975748" /rpt_family="AT_rich"

complement(9379_.9851)

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/note="Region similar to: Hs#S1816152 hd44d11.x1 Homo
/note="Region similar"
9770. 10043

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12336. 12639 /rpt_family="Alusc" complement(13047. .13192) /rpt_family="MIR" complement(131910. .14180) /note="Region similar to: Hs#S1034663 om10h11.s1 Homo sapiens cDNA: AA907068" preferred partner (LPP) gene" 5449. .6622 complement(14381..14842) /rpt_family="L1PA3" 14843..15191 /rpt_family="A-rich"
8121. .8205
/rpt_family="CT-rich"
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Length: 14 Length: 14 Dercent Similarity: 85.714 Percent Identity: 57.143 Lignment Flact
                     /rpt_family="Alusq"
21804. 21912
/rpt_family="Ind"
/rpt_family="Ind"
21913. 21989
/rpt_family="(TA)n"
21990. 22716
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31541. 31633
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7rpt_family="MER20"
31990. 32040
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24159. 24468
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25419. 25705
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25982. .26254
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/rpt_family="AluSg"
34159. .34213
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/rpt_family="L2"
complement(21429, .21723)
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23175. .23407
/rpt_family="AluSq"
23446. .23726
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23767. .23831
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/rpt_family="L1M4"
22720. .22894
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complement(25706.
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26602. .26657
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